GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 12, 2004, 14:01:27 ; Search time 2154 Seconds
(without alignments)
12638.093 Million cell updates/sec

Title: US-09-996-128A-1
Perfect score: 6408
Sequence: 1 attctgcagatatccagcac.....tcttattttaaaaaaccgga 6408

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	6408	100.0	6408	7	ABX10643	Abx10643 Vector, h
2	5636	88.0	6485	7	ABX10644	Abx10644 Vector, h
c 3	2878.4	44.9	5386	9	ADD35598	Add35598 Bicistron
c 4	2878.4	44.9	7086	9	ADD35600	Add35600 Tricistro
c 5	2878.4	44.9	7334	9	ADD35601	Add35601 Tetracist
6	2378.8	37.1	5089	7	ABZ59287	Abz59287 Plasmid p
7	2378.8	37.1	5089	7	ABZ59290	Abz59290 Plasmid p
8	2378.8	37.1	5488	7	ABZ59291	Abz59291 Plasmid p
9	2378.8	37.1	5488	7	ABZ59288	Abz59288 Plasmid p
10	2378.8	37.1	5500	7	ABZ59289	Abz59289 Plasmid p
11	2378.8	37.1	5500	7	ABZ59286	Abz59286 Plasmid p
12	2027.6	31.6	10466	9	ADE06467	Ade06467 Vector pG
13	2027.6	31.6	10466	9	ADE06466	Ade06466 Vector pG
14	2027.2	31.6	10447	9	ADE06463	Ade06463 Vector pG
15	2027.2	31.6	10447	9	ADE06462	Ade06462 Vector pG
16	2020.8	31.5	9918	6	AAS19260	Aas19260 DNA vacci
17	2008.6	31.3	5108	4	AAC86259	Aac86259 Plasmid G
18	2008.6	31.3	5108	4	AAC86258	Aac86258 Plasmid G
19	2008.6	31.3	5108	6	ABK53269	Abk53269 Growth ho
20	2008.6	31.3	5108	6	ABK53270	Abk53270 Growth ho
21	2008.6	31.3	5111	4	AAC86262	Aac86262 CMV IE pr
22	2008.6	31.3	5111	6	ABK53273	Abk53273 Growth ho
23	2008.6	31.3	5185	4	AAC86254	Aac86254 pGHRH-4 c
24	2008.6	31.3	5185	6	ABK53265	Abk53265 Growth ho
25	2008.6	31.3	5188	4	AAC86266	Aac86266 Plasmid G
26	2008.6	31.3	5188	6	ABK53277	Abk53277 Growth ho
27	2008.6	31.3	5254	4	AAC86267	Aac86267 Plasmid p
28	2008.6	31.3	5254	6	ABK85601	Abk85601 Growth ho
29	2005.8	31.3	10447	9	ADE06464	Ade06464 Vector pG
30	1993.8	31.1	10446	9	ADE06465	Ade06465 Vector pG
31	1965.2	30.7	5899	7	ABS55905	Abs55905 DNA plasm
32	1955.6	30.5	7528	4	AAF30316	Aaf30316 Bicistron
33	1942.2	30.3	5843	2	AAV00676	Aav00676 DNA plasm
34	1942.2	30.3	5845	7	ABS55904	Abs55904 DNA plasm
35	1925.4	30.0	5898	2	AAV00677	Aav00677 DNA plasm
36	1892.6	29.5	2041	4	AAS60958	Aas60958 Human can
37	1892.4	29.5	1894	2	AAQ06552	Aaq06552 Clone BBT
38	1890.8	29.5	1894	2	AAT01009	Aat01009 Human tyr
39	1890.8	29.5	1894	2	AAT75678	Aat75678 Human SK2
40	1886.6	29.4	1964	7	ABQ83843	Abq83843 Human tyr
41	1886.6	29.4	1964	9	ADC09569	Adc09569 Tyrosinas
42	1886.6	29.4	2384	2	AAT33316	Aat33316 Tyrosinas
43	1886.6	29.4	2384	2	ABQ76197	Abq76197 Human tum
44	1885	29.4	1906	2	AAQ66548	Aaq66548 Human tyr
45	1885	29.4	1910	2	AAT35901	Aat35901 Tyrosinas

ALIGNMENTS

RESULT 1
ABX10643
ID ABX10643 standard; DNA; 6408 BP.
XX
AC ABX10643;
XX
DT 22-APR-2003 (first entry)
XX
DE Vector, htyr-pING, containing human tyrosinase gene.
XX
KW Human; gene; ds; melanoma; xenogeneic differentiation antigen; DA; pING;
KW tyrosinase; canine; gene therapy; dog; cytostatic.
XX
OS Homo sapiens.
XX
PN US2002150589-A1.
XX
PD 17-OCT-2002.
XX
PF 27-NOV-2001; 2001US-00996128.
XX
PR 10-DEC-1996; 96US-0032535P.
PR 18-FEB-1997; 97US-0036419P.
PR 10-DEC-1997; 97WO-US022669.
PR 21-MAY-1999; 99US-00308697.
PR 26-JAN-2000; 2000US-0180651P.
PR 28-JUL-2000; 2000US-00627694.
XX
PA (HOUG/) HOUGHTON A N.
PA (BERG/) BERGMAN P J.
PA (WOLC/) WOLCHOK J D.
XX
PI Houghton AN, Bergman PJ, Wolchok JD;
XX
DR WPI; 2003-182484/18.
XX
PT Treating melanoma in a mammalian subject comprises administering to the
PT subject an immunological amount of a xenogeneic differentiation antigen
PT of the same type as a differentiation antigen expressed by melanoma cells
PT of the subject.
XX
PS Claim 26; Page 5-8; 15pp; English.
XX
CC The invention discloses a method for treating melanoma in a mammalian
CC subject which comprises administering to the subject an immunological
CC amount of a xenogeneic differentiation antigen (DA) of the same type as a

CC DA expressed by melanoma cells of the subject. Also disclosed are pING
CC vectors containing a sequence encoding the human or mouse tyrosinase
CC genes. The methods and xenogeneic DA are useful for treating canine
CC malignant melanoma (gene therapy) in dog suffering from the disease by
CC administering an immunological amount of the xenogeneic DA and for other
CC mammals. The sequence presented is the vector, htyr-pING, containing the
CC human tyrosinase gene
XX
SQ Sequence 6408 BP; 1621 A; 1583 C; 1509 G; 1695 T; 0 U; 0 Other;

Query Match 100.0%; Score 6408; DB 7; Length 6408;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 6408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATTCTGCAGATATCCAGCACAGTGGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTCTGCAGATATCCAGCACAGTGGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCG 60

Qy         61 CTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGT 120

Qy        121 GCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT 180

Qy        181 TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG 240

Qy        241 CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGGTGGGGATGCAGGGGGGGGGGGGCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGGTGGGGATGCAGGGGGGGGGGGGCG 300

Qy        301 CTGAGGTCTGCCTCGTGAAGAAGGTGTTGCTGACTCATACCAGGCCTGAATCGCCCCATC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAGGTCTGCCTCGTGAAGAAGGTGTTGCTGACTCATACCAGGCCTGAATCGCCCCATC 360

Qy        361 ATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGAGCTTTGTTGTAGGTGGACCAGTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGAGCTTTGTTGTAGGTGGACCAGTT 420

Qy        421 GGTGATTTTGAACTTTTGCTTTGCCACGGAACGGTCTGCGTTGTCGGGAAGATGCGTGAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGATTTTGAACTTTTGCTTTGCCACGGAACGGTCTGCGTTGTCGGGAAGATGCGTGAT 480

Qy        481 CTGATCCTTCAACTCAGCAAAAGTTCGATTTATTCAACAAAGCCGCCGTCCCGTCAAGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGATCCTTCAACTCAGCAAAAGTTCGATTTATTCAACAAAGCCGCCGTCCCGTCAAGTC 540

Qy        541 AGCGTAATGCTCTGCCAGTGTTACAACCAATTAACCAATTCTGATTAGAAAAACTCATCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCGTAATGCTCTGCCAGTGTTACAACCAATTAACCAATTCTGATTAGAAAAACTCATCG 600

Qy        601 AGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAA 660

Qy        661 AGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCC 720

Qy        721 TGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCG 780

Qy        781 TCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAAT 840

Qy        841 GGCAAAAGCTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCAAAAGCTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCA 900

Qy        901 TCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGA 960

Qy        961 AATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGG 1020

Qy       1021 AACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGG 1080

Qy       1081 AATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATA 1140

Qy       1141 AAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCA 1200

Qy       1201 TCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCG 1260

Qy       1261 GGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCAT 1320

Qy       1321 TTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTCGAGCAAGACGTT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTCGAGCAAGACGTT 1380

Qy       1381 TCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTATGTAAGCAGACAGTTTT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTATGTAAGCAGACAGTTTT 1440

Qy       1441 ATTGTTCATGATGATATATTTTTATCTTGTGCAATGTAACATCAGAGATTTTGAGACACA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 ATTGTTCATGATGATATATTTTTATCTTGTGCAATGTAACATCAGAGATTTTGAGACACA 1500

Qy       1501 ACGTGGCTTTCCCCCCCCCCCCTGCAGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 ACGTGGCTTTCCCCCCCCCCCCTGCAGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAG 1560

Qy       1561 TTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTC 1620

Qy       1621 AGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTA 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 AGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTA 1680

Qy       1681 GGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCA 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 GGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCA 1740

Qy       1741 CTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCG 1800

Qy       1801 CGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 CGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGA 1860

Qy       1861 TCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAA 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 TCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAA 1920

Qy       1921 TACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCC 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCC 1980
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Qy       1981 TACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTG 2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 TACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTG 2040

Qy       2041 TCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAAC 2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 TCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAAC 2100

Qy       2101 GGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCT 2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 GGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCT 2160

Qy       2161 ACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCC 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 ACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCC 2220

Qy       2221 GGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 GGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTG 2280

Qy       2281 GTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATG 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATG 2340

Qy       2341 CTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 CTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCT 2400

Qy       2401 GGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2401 GGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGA 2460

Qy       2461 TAACCGTATTACCGCCATGCATTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2461 TAACCGTATTACCGCCATGCATTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTC 2520

Qy       2521 ATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGAC 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 ATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGAC 2580

Qy       2581 CGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGAGATCTGATATAGGTGACAGAC 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 CGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGAGATCTGATATAGGTGACAGAC 2640

Qy       2641 GATATGAGGCTATATCGCCGATAGAGGCGACATCAAGCTGGCACATGGCCAATGCATATC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 GATATGAGGCTATATCGCCGATAGAGGCGACATCAAGCTGGCACATGGCCAATGCATATC 2700

Qy       2701 GATCTATACATTGAATCAATATTGGCAATTAGCCATATTAGTCATTGGTTATATAGCATA 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 GATCTATACATTGAATCAATATTGGCAATTAGCCATATTAGTCATTGGTTATATAGCATA 2760

Qy       2761 AATCAATATTGGCTATTGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTA 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 AATCAATATTGGCTATTGGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTA 2820

Qy       2821 TATTGGCTCATGTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATA 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 TATTGGCTCATGTCCAATATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATA 2880

Qy       2881 GTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACT 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 GTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACT 2940

Qy       2941 TACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATGAT 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 TACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATGAT 3000

Qy       3001 GACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTA 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3001 GACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTA 3060

Qy       3061 TTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCC 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3061 TTTACGGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCC 3120

Qy       3121 TATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3121 TATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACG 3180

Qy       3181 GGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCG 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3181 GGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCG 3240

Qy       3241 GTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCT 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3241 GTTTTGGCAGTACACCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCT 3300

Qy       3301 CCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAA 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3301 CCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAA 3360

Qy       3361 ATGTCGTAATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGT 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3361 ATGTCGTAATAACCCCGCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGT 3420

Qy       3421 CTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTG 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3421 CTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTG 3480

Qy       3481 TTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCAT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3481 TTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCAT 3540

Qy       3541 TGGAACGCGGATTCCCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCA 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3541 TGGAACGCGGATTCCCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCA 3600

Qy       3601 CACCCCTTTGGCTCTTATGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCCGC 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3601 CACCCCTTTGGCTCTTATGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCCGC 3660

Qy       3661 TTCCTTATGCTATAGGTGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTAT 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3661 TTCCTTATGCTATAGGTGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTAT 3720

Qy       3721 TGACCACTCCCCTATTGGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGC 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 TGACCACTCCCCTATTGGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGC 3780

Qy       3781 CACAACTATCTCTATTGGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTC 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 CACAACTATCTCTATTGGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTC 3840

Qy       3841 TGTATTTTTACAGGATGGGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCC 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 TGTATTTTTACAGGATGGGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCC 3900

Qy       3901 GTCCCCCGTGCCCGCAGTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGT 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 GTCCCCCGTGCCCGCAGTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGT 3960

Qy       3961 ACGTGTTCCGGACATGGGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGG 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 ACGTGTTCCGGACATGGGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGG 4020

Qy       4021 TCCCATGCCTCCAGCGGCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCC 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 TCCCATGCCTCCAGCGGCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCC 4080

Qy       4081 AGACTTAGGCACAGCACAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTA 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 AGACTTAGGCACAGCACAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTA 4140

Qy       4141 GGGTATGTGTCTGAAAATGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGA 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       4141 GGGTATGTGTCTGAAAATGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGA 4200
Qy       4201 CTTAAGGCAGCGGCAGAAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCA 4260
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 CTTAAGGCAGCGGCAGAAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCA 4260

Qy       4261 GAGGTAACTCCCGTTGCGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTC 4320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 GAGGTAACTCCCGTTGCGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTC 4320

Qy       4321 GTTGCTGCCGCGCGCGCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCC 4380
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 GTTGCTGCCGCGCGCGCCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCC 4380

Qy       4381 ATGGGTCTTTTCTGCAGTCACCGTCCACGCGTTAATACGACTCACTATAGGGAGACCCAA 4440
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 ATGGGTCTTTTCTGCAGTCACCGTCCACGCGTTAATACGACTCACTATAGGGAGACCCAA 4440

Qy       4441 GCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCACTAGTCCAGTGTGGT 4500
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCACTAGTCCAGTGTGGT 4500

Qy       4501 GGAATTCCGGGAAGAATGCTCCTGGCTGTTTTGTACTGCCTGCTGTGGAGTTTCCAGACC 4560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 GGAATTCCGGGAAGAATGCTCCTGGCTGTTTTGTACTGCCTGCTGTGGAGTTTCCAGACC 4560

Qy       4561 TCCGCTGGCCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAGAAGGAATGC 4620
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 TCCGCTGGCCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAGAAGGAATGC 4620

Qy       4621 TGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGAGGTTCCTGT 4680
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4621 TGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGAGGTTCCTGT 4680

Qy       4681 CAGAATATCCTTCTGTCCAATGCACCACTTGGGCCTCAATTTCCCTTCACAGGGGTGGAT 4740
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4681 CAGAATATCCTTCTGTCCAATGCACCACTTGGGCCTCAATTTCCCTTCACAGGGGTGGAT 4740

Qy       4741 GACCGGGAGTCGTGGCCTTCCGTCTTTTATAATAGGACCTGCCAGTGCTCTGGCAACTTC 4800
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4741 GACCGGGAGTCGTGGCCTTCCGTCTTTTATAATAGGACCTGCCAGTGCTCTGGCAACTTC 4800

Qy       4801 ATGGGATTCAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGAGAGA 4860
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4801 ATGGGATTCAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGAGAGA 4860

Qy       4861 CGACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATTTTTT 4920
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4861 CGACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATTTTTT 4920

Qy       4921 GCCTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGGGACC 4980
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4921 GCCTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGGGACC 4980

Qy       4981 TATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGACCTC 5040
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4981 TATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGACCTC 5040

Qy       5041 TTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATATGAAATCTGG 5100
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5041 TTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATATGAAATCTGG 5100

Qy       5101 AGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTTCTTG 5160
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5101 AGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTTCTTG 5160

Qy       5161 TTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACTATTCCATAT 5220
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5161 TTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACTATTCCATAT 5220

Qy       5221 TGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAG 5280
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5221 TGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAG 5280
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Qy       5281 CACCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCAGATTGTC 5340
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5281 CACCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCAGATTGTC 5340

Qy       5341 TGTAGCCGATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGAACGCCCGAGGGA 5400
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5341 TGTAGCCGATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGAACGCCCGAGGGA 5400

Qy       5401 CCTTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTCCCCTCTTCA 5460
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5401 CCTTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTCCCCTCTTCA 5460

Qy       5461 GCTGATGTAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGTTCCATGGATAAAGCT 5520
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5461 GCTGATGTAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGTTCCATGGATAAAGCT 5520

Qy       5521 GCCAATTTCAGCTTTAGAAATACACTGGAAGGATTTGCTAGTCCACTTACTGGGATAGCG 5580
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5521 GCCAATTTCAGCTTTAGAAATACACTGGAAGGATTTGCTAGTCCACTTACTGGGATAGCG 5580

Qy       5581 GATGCCTCTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAATGGAACAATGTCC 5640
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5581 GATGCCTCTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAATGGAACAATGTCC 5640

Qy       5641 CAGGTACAGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCATGCATTTGTTGACAGT 5700
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5641 CAGGTACAGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCATGCATTTGTTGACAGT 5700

Qy       5701 ATTTTTGAGCAGTGGCTCCGAAGGCACCGTCCTCTTCAAGAAGTTTATCCAGAAGCCAAT 5760
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5701 ATTTTTGAGCAGTGGCTCCGAAGGCACCGTCCTCTTCAAGAAGTTTATCCAGAAGCCAAT 5760

Qy       5761 GCACCCATTGGACATAACCGGGAATCCTACATGGTTCCTTTTATACCACTGTACAGAAAT 5820
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5761 GCACCCATTGGACATAACCGGGAATCCTACATGGTTCCTTTTATACCACTGTACAGAAAT 5820

Qy       5821 GGTGATTTCTTTATTTCATCCAAAGATCTGGGCTATGACTATAGCTATCTACAAGATTCA 5880
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5821 GGTGATTTCTTTATTTCATCCAAAGATCTGGGCTATGACTATAGCTATCTACAAGATTCA 5880

Qy       5881 GACCCAGACTCTTTTCAAGACTACATTAAGTCCTATTTGGAACAAGCGAGTCGGATCTGG 5940
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5881 GACCCAGACTCTTTTCAAGACTACATTAAGTCCTATTTGGAACAAGCGAGTCGGATCTGG 5940

Qy       5941 TCATGGCTCCTTGGGGCGGCGATGGTAGGGGCCGTCCTCACTGCCCTGCTGGCAGGGCTT 6000
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5941 TCATGGCTCCTTGGGGCGGCGATGGTAGGGGCCGTCCTCACTGCCCTGCTGGCAGGGCTT 6000

Qy       6001 GTGAGCTTGCTGTGTCGTCACAAGAGAAAGCAGCTTCCTGAAGAAAAGCAGCCACTCCTC 6060
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6001 GTGAGCTTGCTGTGTCGTCACAAGAGAAAGCAGCTTCCTGAAGAAAAGCAGCCACTCCTC 6060

Qy       6061 ATGGAGAAAGAGGATTACCACAGCTTGTATCAGAGCCATTTATAAAAGGCTTAGGCAATA 6120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6061 ATGGAGAAAGAGGATTACCACAGCTTGTATCAGAGCCATTTATAAAAGGCTTAGGCAATA 6120

Qy       6121 GAGTAGGGCCAAAAAGCCTGACCTCACTCTAACTCAAAGTAATGTCCAGGTTCCCAGAGA 6180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6121 GAGTAGGGCCAAAAAGCCTGACCTCACTCTAACTCAAAGTAATGTCCAGGTTCCCAGAGA 6180

Qy       6181 ATATCTGCTGGTATTTTTCTGTAAAGACCATTTGCAAAATTGTAACCTAATACAAAGTGT 6240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6181 ATATCTGCTGGTATTTTTCTGTAAAGACCATTTGCAAAATTGTAACCTAATACAAAGTGT 6240

Qy       6241 AGCCTTCTTCCAACTCAGGTAGAACACACCTGTCTTTGTCTTGCTGTTTTCACTCAGCCC 6300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 AGCCTTCTTCCAACTCAGGTAGAACACACCTGTCTTTGTCTTGCTGTTTTCACTCAGCCC 6300

Qy       6301 TTTTAACATTTTCCCCTAAGCCCATATGTCTAAGGAAAGGATGCTATTTGGTAATGAGGA 6360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 TTTTAACATTTTCCCCTAAGCCCATATGTCTAAGGAAAGGATGCTATTTGGTAATGAGGA 6360
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Qy       6361 ACTGTTATTTGTATGTGAATTAAAGTGCTCTTATTTTAAAAAACCGGA 6408
             ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 ACTGTTATTTGTATGTGAATTAAAGTGCTCTTATTTTAAAAAACCGGA 6408
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RESULT 2
ABX10644
ID ABX10644 standard; DNA; 6485 BP.
XX
AC ABX10644;
XX
DT 22-APR-2003 (first entry)
XX
DE Vector, htyr-pING, containing mouse tyrosinase gene.
XX
KW Mouse; gene; ds; melanoma; xenogeneic differentiation antigen; DA; pING;
KW tyrosinase; canine; gene therapy; dog; cytostatic.
XX
OS Mus sp.
XX
PN US2002150589-A1.
XX
PD 17-OCT-2002.
XX
PF 27-NOV-2001; 2001US-00996128.
XX
PR 10-DEC-1996; 96US-0032535P.
PR 18-FEB-1997; 97US-0036419P.
PR 10-DEC-1997; 97WO-US022669.
PR 21-MAY-1999; 99US-00308697.
PR 26-JAN-2000; 2000US-0180651P.
PR 28-JUL-2000; 2000US-00627694.
XX
PA (HOUG/) HOUGHTON A N.
PA (BERG/) BERGMAN P J.
PA (WOLC/) WOLCHOK J D.
XX
PI Houghton AN, Bergman PJ, Wolchok JD;
XX
DR WPI; 2003-182484/18.
XX
PT Treating melanoma in a mammalian subject comprises administering to the
PT subject an immunological amount of a xenogeneic differentiation antigen
PT of the same type as a differentiation antigen expressed by melanoma cells
PT of the subject.
XX
PS Claim 27; Page 8-11; 15pp; English.
XX
CC The invention discloses a method for treating melanoma in a mammalian
CC subject which comprises administering to the subject an immunological
CC amount of a xenogeneic differentiation antigen (DA) of the same type as a
CC DA expressed by melanoma cells of the subject. Also disclosed are pING
CC vectors containing a sequence encoding the human or mouse tyrosinase
CC genes. The methods and xenogeneic DA are useful for treating canine
CC malignant melanoma (gene therapy) in dog suffering from the disease by
CC administering an immunological amount of the xenogeneic DA and for other
CC mammals. The sequence presented is the vector, htyr-pING, containing the
CC mouse tyrosinase gene
XX
SQ Sequence 6485 BP; 1658 A; 1570 C; 1504 G; 1753 T; 0 U; 0 Other;

Query Match 88.0%; Score 5636; DB 7; Length 6485;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 5884; Conservative 0; Mismatches 270; Indels 56; Gaps 3;

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Qy          1 ATTCTGCAGATATCCAGCACAGTGGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATTCTGCAGATATCCAGCACAGTGGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCG 60

Qy         61 CTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCTCCCCCGT 120

Qy        121 GCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAAT 180

Qy        181 TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAG 240

Qy        241 CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGGTGGGGATGCAGGGGGGGGGGGGCG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAAGGGGGAGGATTGGGAAGACAATAGCAGGCATGGTGGGGATGCAGGGGGGGGGGGGCG 300

Qy        301 CTGAGGTCTGCCTCGTGAAGAAGGTGTTGCTGACTCATACCAGGCCTGAATCGCCCCATC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAGGTCTGCCTCGTGAAGAAGGTGTTGCTGACTCATACCAGGCCTGAATCGCCCCATC 360

Qy        361 ATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGAGCTTTGTTGTAGGTGGACCAGTT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGAGCTTTGTTGTAGGTGGACCAGTT 420

Qy        421 GGTGATTTTGAACTTTTGCTTTGCCACGGAACGGTCTGCGTTGTCGGGAAGATGCGTGAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGATTTTGAACTTTTGCTTTGCCACGGAACGGTCTGCGTTGTCGGGAAGATGCGTGAT 480

Qy        481 CTGATCCTTCAACTCAGCAAAAGTTCGATTTATTCAACAAAGCCGCCGTCCCGTCAAGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGATCCTTCAACTCAGCAAAAGTTCGATTTATTCAACAAAGCCGCCGTCCCGTCAAGTC 540

Qy        541 AGCGTAATGCTCTGCCAGTGTTACAACCAATTAACCAATTCTGATTAGAAAAACTCATCG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGCGTAATGCTCTGCCAGTGTTACAACCAATTAACCAATTCTGATTAGAAAAACTCATCG 600

Qy        601 AGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAA 660

Qy        661 AGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCC 720

Qy        721 TGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCG 780

Qy        781 TCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAAT 840

Qy        841 GGCAAAAGCTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GGCAAAAGCTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCA 900

Qy        901 TCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGA 960

Qy        961 AATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGG 1020

Qy       1021 AACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGG 1080
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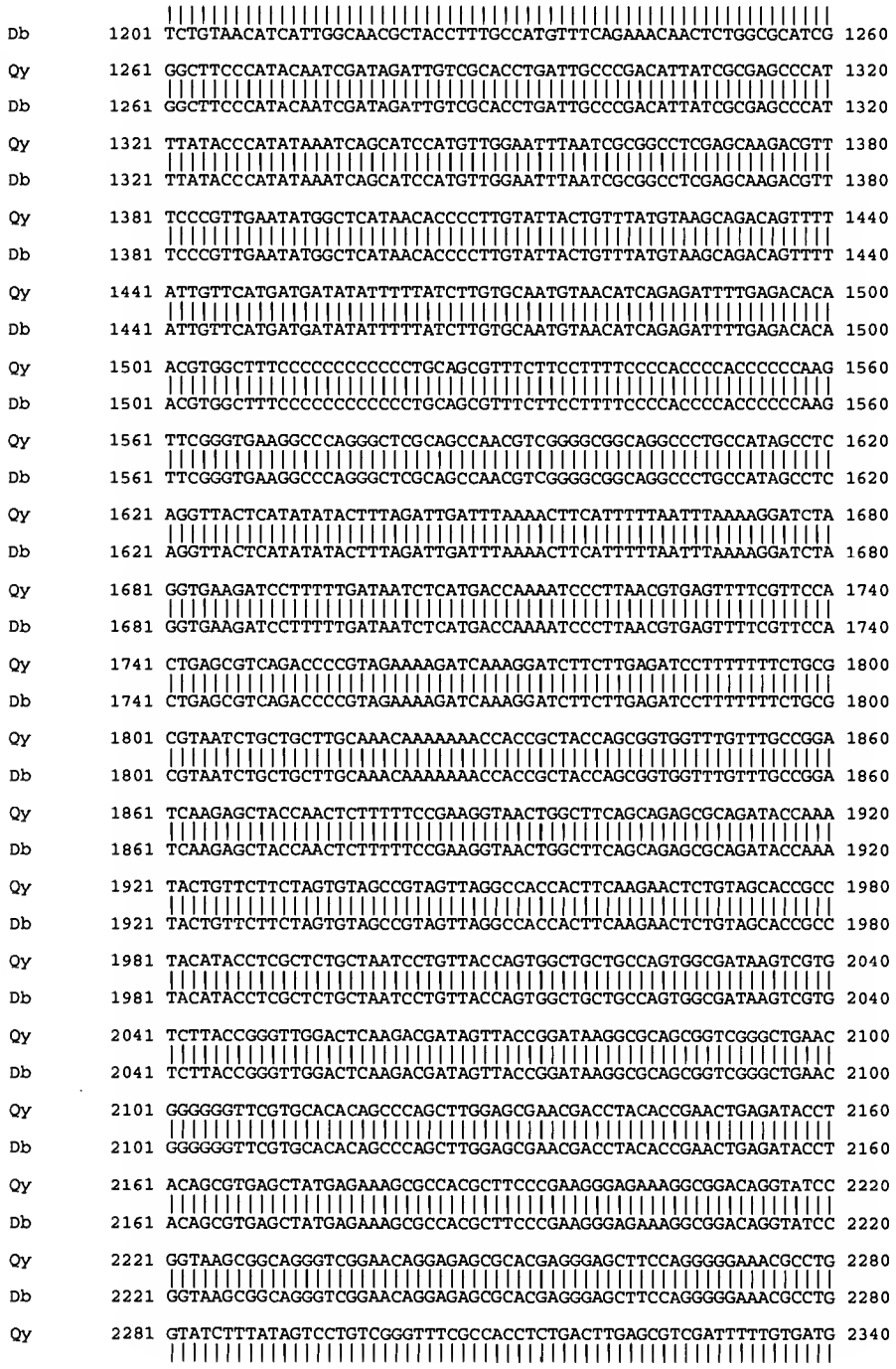
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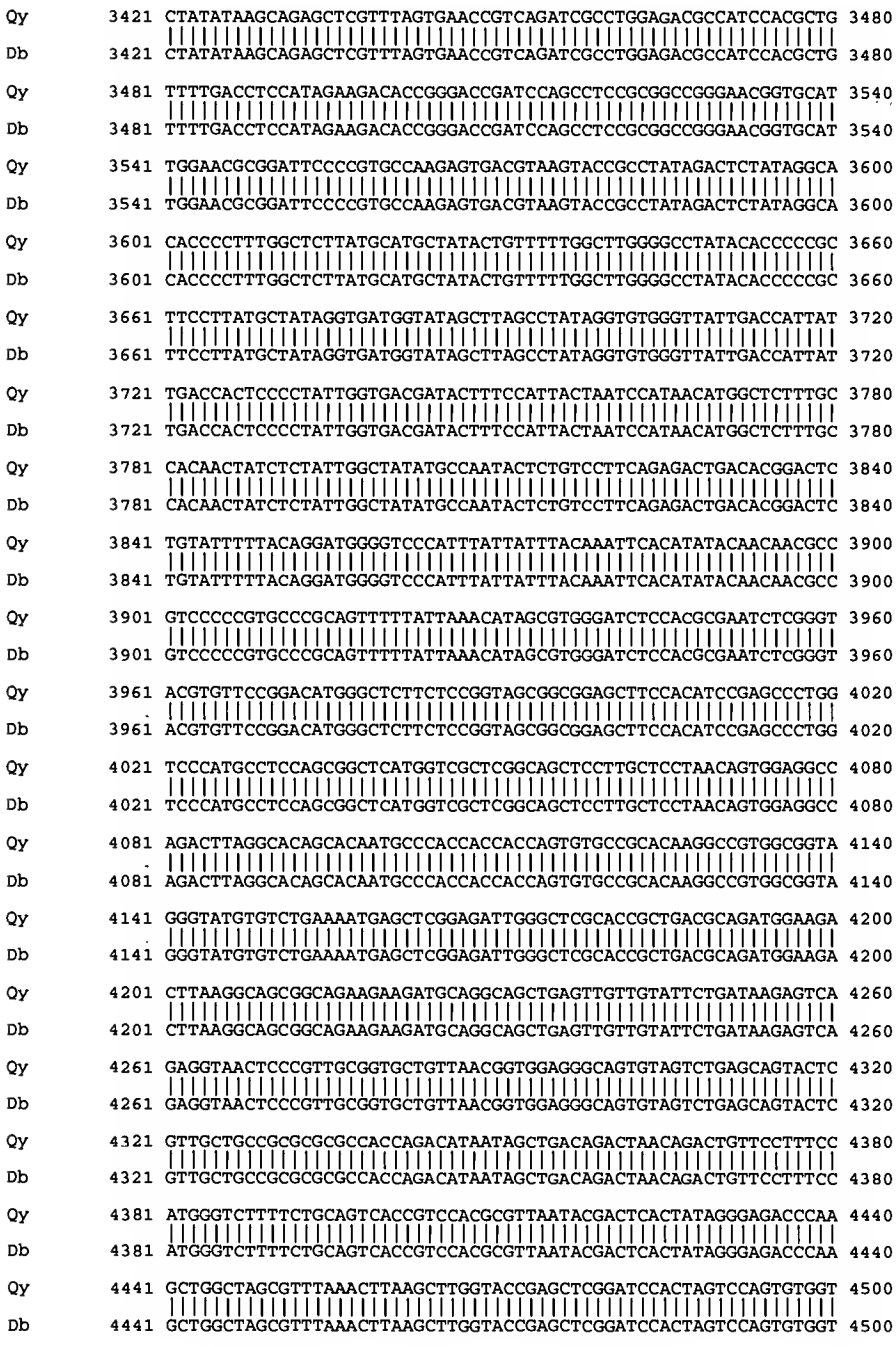
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RESULT 3
ADD35598/c

ID ADD35598 standard; DNA; 5386 BP.
XX
AC ADD35598;
XX
DT 15-JAN-2004 (first entry)
XX
DE Bicistronic eukaryotic expression vector PL190.
XX
KW Multicistronic eukaryotic expression vector; multiple protein expression;
KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
KW chain terminator; transcription pause site; gene transfer;
KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;
KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site; cyclic;
KW circular; ds.
XX
OS Chimeric.
OS Synthetic.
OS Human herpesvirus 5.
OS Encephalomyocarditis virus.
OS Simian virus 40.
OS Escherichia coli.
XX
PN WO2003031630-A1.
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002WO-IT000646.
XX
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XX
PA (KERY-) KERYOS SPA.
XX
PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
XX
DR WPI; 2003-393446/37.
XX
PT New multicistronic recombinant plasmid vectors expressing two to our
PT genes simultaneously, useful in various biotechnological applications,
PT such as gene transfer, gene therapy and in DNA immunization.
XX
PS Claim 18; SEQ ID NO 1; 52pp; English.
XX
CC The invention relates to multicistronic eukaryotic expression vectors for
CC the expression of at least two proteins of interest which may be
CC identical or different. The vectors comprise at least one eukaryotic
CC expression cassette having a promoter/enhancer sequence, an intron
CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
CC and a chain terminator. The vectors may additionally contain a
CC transcription pause site downstream of the chain terminator. The
CC invention also encompasses eukaryotic host cells comprising a vector of
CC the invention, and the recombinant expression of two or more eukaryotic
CC proteins using host cells transformed with a vectopr of the invention.
CC The vectors are useful in various biotechnological applications in which
CC the simultaneous expression of two or more genes is necessary, such as
CC gene transfer protocols, DNA immunisation, or for the expression of
CC different molecules in the same cell. They may also be used in gene
CC therapy. The present sequence represents a specifically claimed vector
CC designated PL190, which comprises a cytomegalovirus (CMV)
CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
CC IRES, an SV40 polyadenylation site and a transcription pause site, as
CC well as a kanamycin resistance gene.
XX
SQ Sequence 5386 BP; 1353 A; 1307 C; 1386 G; 1340 T; 0 U; 0 Other;

Query Match 44.9%; Score 2878.4; DB 9; Length 5386;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;

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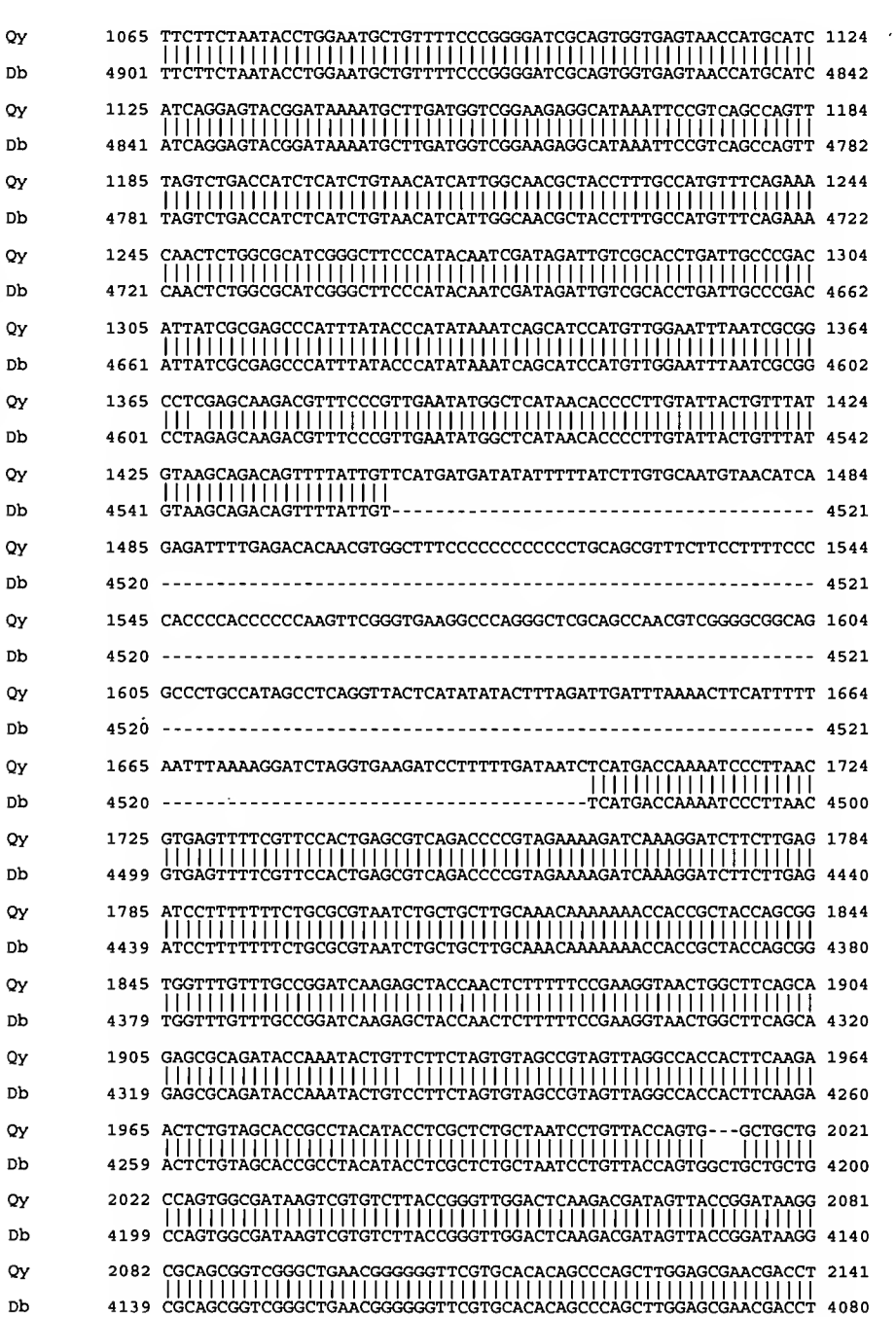
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Qy 1245 CAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC 1304
Db 4721 CAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC 4662
Qy 1305 ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGG 1364
Db 4661 ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGG 4602
Qy 1365 CCTCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTAT 1424
Db 4601 CCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTAT 4542
Qy 1425 GTAAGCAGACAGTTTTATTGTTCATGATGATATATTTTTATCTTGTGCAATGTAACATCA 1484
Db 4541 GTAAGCAGACAGTTTTATTGT---------- 4521
Qy 1485 GAGATTTTGAGACACAACGTGGCTTTCCCCCCCCCCCCTGCAGCGTTTCTTCCTTTTCCC 1544
Db 4520 ---------- 4521
Qy 1545 CACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAG 1604
Db 4520 ---------- 4521
Qy 1605 GCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTT 1664
Db 4520 ---------- 4521
Qy 1665 AATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAAC 1724
Db 4520 ----------TCATGACCAAAATCCCTTAAC 4500
Qy 1725 GTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 1784
Db 4499 GTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 4440
Qy 1785 ATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGG 1844
Db 4439 ATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGG 4380
Qy 1845 TGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCA 1904
Db 4379 TGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCA 4320
Qy 1905 GAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGA 1964
Db 4319 GAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGA 4260
Qy 1965 ACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTG---GCTGCTG 2021
Db 4259 ACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCTG 4200
Qy 2022 CCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG 2081
Db 4199 CCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG 4140
Qy 2082 CGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT 2141
Db 4139 CGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT 4080
Qy 2142 ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGA 2201
Db 4079 ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGA 4020
Qy 2202 GAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGC 2261
Db 4019 GAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGC 3960
Qy 2262 TTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTG 2321
Db 3959 TTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTG 3900
Qy 2322 AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG 2381
Db 3899 AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG 3840
Qy 2382 CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGT 2441
Db 3839 CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGT 3780
Qy 2442 TATCCCCTGATTCTGTGGATAACCGTATTACCGCC-ATGCATTAGTTATTAATAGTAATC 2500
Db 3779 TATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCC 3720
Qy 2501 AATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAAC---TTAC 2557
Db 3719 GCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATAC 3660
Qy 2558 GGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGAC 2617
Db 3659 GCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTC 3600
Qy 2618 GAGATCTGATATAGGTGACAGACGATATGAGGCTATATCGCCGATAGAGGCGACATCAAG 2677
Db 3599 CCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGG 3540
Qy 2678 C----------TGGCACATGGCCAATGCATATCGATCTATACATTGAATCAATATTGG-- 2725
Db 3539 CACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGAT 3480
Qy 2726 --CAATTAGCCATATTAGTCATTGGTTATATAGCATAAATCAATATTGGCT------ATT 2777
Db 3479 AACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTGCATGCCTGCAGT 3420
Qy 2778 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2837
Db 3419 GGCCATTGCATACGTTGTATCCATATCATAATATGTACATTTATATTGGCTCATGTCCAA 3360
Qy 2838 TATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGT 2897
Db 3359 CATTACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGT 3300
Qy 2898 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2957
Db 3299 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 3240
Qy 2958 CTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATGATGACGTATGTTCCCATAG 3017
Db 3239 CTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG 3180
Qy 3018 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 3077
Db 3179 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 3120
Qy 3078 ACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGCCCCCCTATTGACGTCAATGACG 3137
Db 3119 ACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACG 3060
Qy 3138 GTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGC 3197
Db 3059 GTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGC 3000
Qy 3198 AGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACCA 3257

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Db       2999 AGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCA 2940

Qy       3258 ATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCA 3317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2939 ATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCA 2880

Qy       3318 ATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCG 3377
             |||||||||||||||||||||||||||||||||||||||||||||||||| ||| |||||||
Db       2879 ATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCG 2820

Qy       3378 CCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTC 3437
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2819 CCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTC 2760

Qy       3438 GTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAA 3497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2759 GTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAA 2700

Qy       3498 GACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCCC 3557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2699 GACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCCC 2640

Qy       3558 GTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTTA 3617
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       2639 GTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCACACCCCTTTGGCTCTTA 2580

Qy       3618 TGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGGT 3677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2579 TGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGGT 2520

Qy       3678 GATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATTG 3737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2519 GATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATTG 2460

Qy       3738 GTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTG 3797
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2459 GTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTG 2400

Qy       3798 GCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGATG 3857
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2399 GCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGATG 2340

Qy       3858 GGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCAG 3917
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2339 GGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCAG 2280

Qy       3918 TTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGG 3977
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2279 TTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGG 2220

Qy       3978 GCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCGG 4037
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2219 GCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCGG 2160

Qy       4038 CTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCAC 4097
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2159 CTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCAC 2100

Qy       4098 AATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAAA 4157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2099 AATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAAA 2040

Qy       4158 TGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAGA 4217
             |||||  |||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       2039 TGAGCGTGGAGATTGGGCTCGCACGGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAGA 1980

Qy       4218 AGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGC 4277
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1979 AGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGC 1920

Qy       4278 GGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCGC 4337
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1919 GGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCGC 1860

Qy       4338 CACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAG 4397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1859 CACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAG 1800
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RESULT 4
ADD35600/c
ID ADD35600 standard; DNA; 7086 BP.
XX
AC ADD35600;
XX
DT 15-JAN-2004 (first entry)
XX
DE Tricistronic eukaryotic expression vector PL249.
XX
KW Multicistronic eukaryotic expression vector; multiple protein expression;
KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
KW chain terminator; transcription pause site; gene transfer;
KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;
KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
KW mRGB terminator; cyclic; circular; ds.
XX
OS Chimeric.
OS Synthetic.
OS Human herpesvirus 5.
OS Encephalomyocarditis virus.
OS Simian virus 40.
OS Rous sarcoma virus.
OS Oryctolagus cuniculus.
OS Escherichia coli.
XX
PN WO2003031630-A1.
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002WO-IT000646.
XX
PR 12-OCT-2001; 2001IT-MI002110.
XX
PA (KERY-) KERYOS SPA.
XX
PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
XX
DR WPI; 2003-393446/37.
XX
PT New multicistronic recombinant plasmid vectors expressing two to our
PT genes simultaneously, useful in various biotechnological applications,
PT such as gene transfer, gene therapy and in DNA immunization.
XX
PS Claim 18; SEQ ID NO 3; 52pp; English.
XX
CC The invention relates to multicistronic eukaryotic expression vectors for
CC the expression of at least two proteins of interest which may be
CC identical or different. The vectors comprise at least one eukaryotic
CC expression cassette having a promoter/enhancer sequence, an intron
CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
CC and a chain terminator. The vectors may additionally contain a
CC transcription pause site downstream of the chain terminator. The
CC invention also encompasses eukaryotic host cells comprising a vector of
CC the invention, and the recombinant expression of two or more eukaryotic
CC proteins using host cells transformed with a vectopr of the invention.
CC The vectors are useful in various biotechnological applications in which
CC the simultaneous expression of two or more genes is necessary, such as
CC gene transfer protocols, DNA immunisation, or for the expression of
CC different molecules in the same cell. They may also be used in gene
CC therapy. The present sequence represents a specifically claimed vector
CC designated PL249, which comprises a cytomegalovirus (CMV)
CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous

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CC   sarcoma virus (RSV) promoter, rabbit beta-globin intron, and a rabbit
CC   beta-globin gene mRGB terminator as well as a kanamycin resistance gene.
XX
SQ   Sequence 7086 BP; 1870 A; 1699 C; 1753 G; 1764 T; 0 U; 0 Other;

  Query Match             44.9%;  Score 2878.4;  DB 9;  Length 7086;
  Best Local Similarity   87.3%;  Pred. No. 0;
  Matches 3354;  Conservative    0;  Mismatches  201;  Indels  285;  Gaps    7;

Qy        585 TTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAAT 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7081 TTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAAT 7022

Qy        645 ACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCA 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       7021 ACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCA 6962

Qy        705 TAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACC 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6961 TAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACC 6902

Qy        765 TATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGAC 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6901 TATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGAC 6842

Qy        825 TGAATCCGGTGAGAATGGCAAAAGCTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCA 884
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db       6841 TGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCA 6782

Qy        885 GCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTG 944
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6781 GCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTG 6722

Qy        945 CGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGA 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 CGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGA 6662

Qy       1005 ATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATA 1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 ATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATA 6602

Qy       1065 TTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATC 1124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 TTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATC 6542

Qy       1125 ATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTT 1184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 ATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTT 6482

Qy       1185 TAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAA 1244
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 TAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAA 6422

Qy       1245 CAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC 1304
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 CAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC 6362

Qy       1305 ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGG 1364
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6361 ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGG 6302

Qy       1365 CCTCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTAT 1424
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 CCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTAT 6242

Qy       1425 GTAAGCAGACAGTTTTATTGTTCATGATGATATATTTTTATCTTGTGCAATGTAACATCA 1484
              |||||||||||||||||||||
Db       6241 GTAAGCAGACAGTTTTATTGT---------------------------------------- 6221

Qy       1485 GAGATTTTGAGACACAACGTGGCTTTCCCCCCCCCCCCTGCAGCGTTTCTTCCTTTTCCC 1544
Db       6220 ------------------------------------------------------------ 6221
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Qy       1545 CACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAG 1604
Db       6220 ------------------------------------------------------------ 6221

Qy       1605 GCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTT 1664
Db       6220 ------------------------------------------------------------ 6221

Qy       1665 AATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAAC 1724
                                                  ||||||||||||||||||||
Db       6220 ----------------------------------------TCATGACCAAAATCCCTTAAC 6200

Qy       1725 GTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 1784
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6199 GTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 6140

Qy       1785 ATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGG 1844
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6139 ATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGG 6080

Qy       1845 TGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCA 1904
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6079 TGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCA 6020

Qy       1905 GAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGA 1964
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db       6019 GAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGA 5960

Qy       1965 ACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTG---GCTGCTG 2021
              |||||||||||||||||||||||||||||||||||||||||||||||||   |||||||
Db       5959 ACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCTG 5900

Qy       2022 CCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG 2081
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5899 CCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG 5840

Qy       2082 CGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT 2141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5839 CGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT 5780

Qy       2142 ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGA 2201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5779 ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGA 5720

Qy       2202 GAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGC 2261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5719 GAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGC 5660

Qy       2262 TTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTG 2321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5659 TTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTG 5600

Qy       2322 AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG 2381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5599 AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG 5540

Qy       2382 CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGT 2441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       5539 CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGT 5480

Qy       2442 TATCCCCTGATTCTGTGGATAACCGTATTACCGCC-ATGCATTAGTTATTAATAGTAATC 2500
              |||||||||||||||||||||||||||||||||||  || | || | ||    | | |
Db       5479 TATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCC 5420

Qy       2501 AATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAAC---TTAC 2557
                 ||          ||  ||  |     | |         ||| | | |   |   |||
Db       5419 GCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATAC 5360

Qy       2558 GGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGAC 2617
              | || | | | ||  ||      | || |          |  || | |   | | |
Db       5359 GCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTC 5300

Qy       2618 GAGATCTGATATAGGTGACAGACGATATGAGGCTATATCGCCGATAGAGGCGACATCAAG 2677
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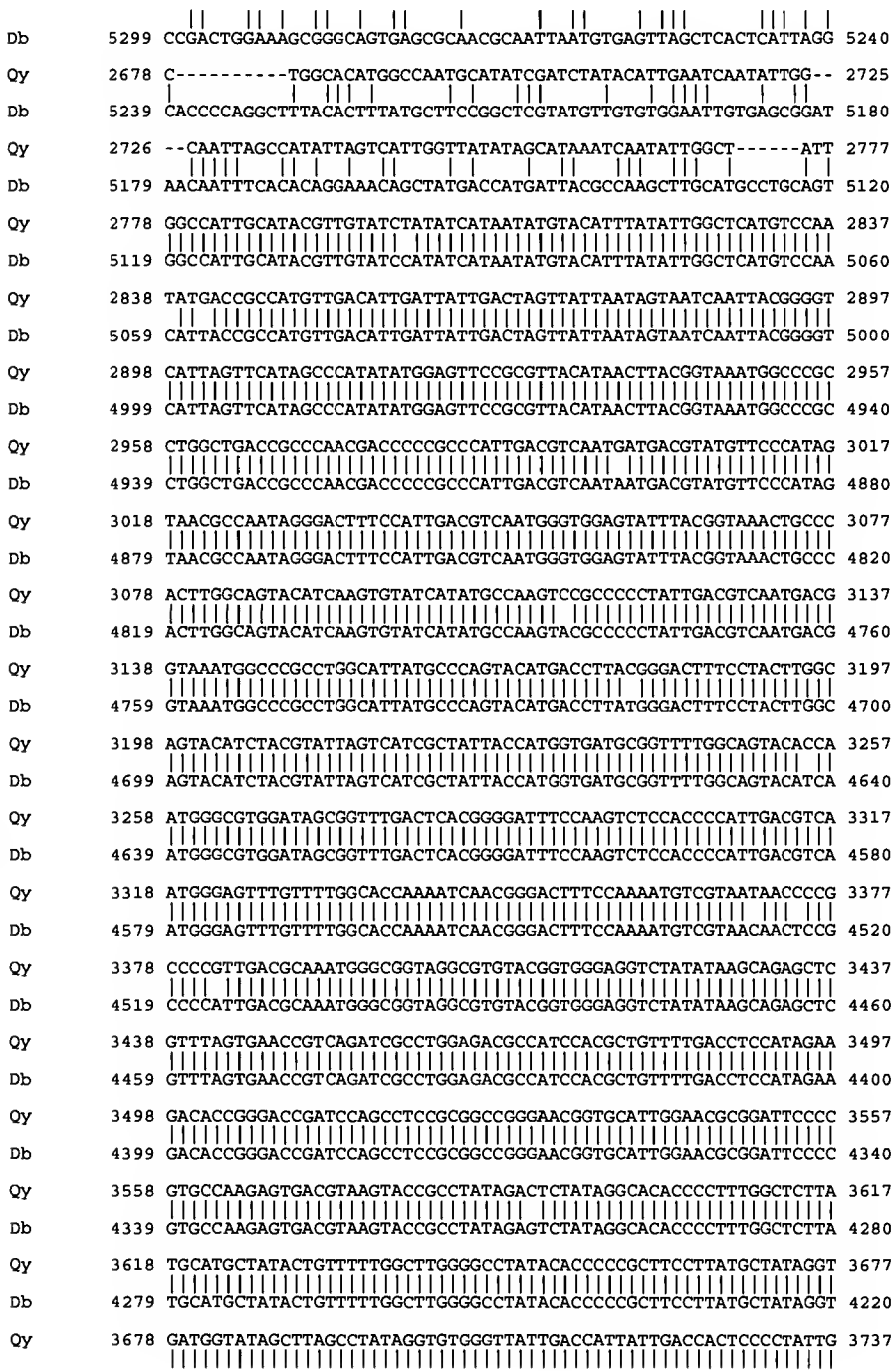

RESULT 5
ADD35601/c
ID ADD35601 standard; DNA; 7334 BP.
XX
AC ADD35601;
XX
DT 15-JAN-2004 (first entry)
XX
DE Tetracistronic eukaryotic expression vector PL250.
XX
KW Multicistronic eukaryotic expression vector; multiple protein expression;
KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
KW chain terminator; transcription pause site; gene transfer;
KW DNA immunisation; gene therapy; PL190; kanamycin resistance gene;
KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
KW encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
KW Rous sarcoma virus; RSV promoter; rabbit beta-globin intron;
KW hepatitis C virus; HCV IRES; mRGB terminator; cyclic; circular; ds.
XX
OS Chimeric.
OS Synthetic.
OS Human herpesvirus 5.
OS Encephalomyocarditis virus.
OS Simian virus 40.
OS Rous sarcoma virus.
OS Oryctolagus cuniculus.

OS Hepatitis C virus.
OS Escherichia coli.
XX
PN WO2003031630-A1.
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002WO-IT000646.
XX
PR 12-OCT-2001; 2001IT-MI002110.
XX
PA (KERY-) KERYOS SPA.
XX
PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
XX
DR WPI; 2003-393446/37.
XX
PT New multicistronic recombinant plasmid vectors expressing two to our
PT genes simultaneously, useful in various biotechnological applications,
PT such as gene transfer, gene therapy and in DNA immunization.
XX
PS Claim 18; SEQ ID NO 4; 52pp; English.
XX
CC The invention relates to multicistronic eukaryotic expression vectors for
CC the expression of at least two proteins of interest which may be
CC identical or different. The vectors comprise at least one eukaryotic
CC expression cassette having a promoter/enhancer sequence, an intron
CC sequence, a cloning site, a viral internal ribosomal entry site (IRES)
CC and a chain terminator. The vectors may additionally contain a
CC transcription pause site downstream of the chain terminator. The
CC invention also encompasses eukaryotic host cells comprising a vector of
CC the invention, and the recombinant expression of two or more eukaryotic
CC proteins using host cells transformed with a vectopr of the invention.
CC The vectors are useful in various biotechnological applications in which
CC the simultaneous expression of two or more genes is necessary, such as
CC gene transfer protocols, DNA immunisation, or for the expression of
CC different molecules in the same cell. They may also be used in gene
CC therapy. The present sequence represents a specifically claimed vector
CC designated PL250, which comprises a cytomegalovirus (CMV)
CC promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
CC IRES, an SV40 polyadenylation site, a transcription pause site, a Rous
CC sarcoma virus (RSV) promoter, rabbit beta-globin intron, the hepatitis C
CC virus (HCV) IRES, and a rabbit beta-globin gene mRGB terminator as well
CC as a kanamycin resistance gene.
XX
SQ Sequence 7334 BP; 1922 A; 1775 C; 1825 G; 1812 T; 0 U; 0 Other;

Query Match 44.9%; Score 2878.4; DB 9; Length 7334;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 3354; Conservative 0; Mismatches 201; Indels 285; Gaps 7;

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Qy       585 TTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAAT 644
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7329 TTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAAT 7270

Qy       645 ACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCA 704
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7269 ACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCA 7210

Qy       705 TAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACC 764
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7209 TAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACC 7150

Qy       765 TATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGAC 824
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7149 TATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGAC 7090

Qy       825 TGAATCCGGTGAGAATGGCAAAAGCTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCA 884
            |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db      7089 TGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCA 7030

Qy       885 GCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTG 944
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      7029 GCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTG 6970

Qy       945 CGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGA 1004
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6969 CGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGA 6910

Qy      1005 ATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATA 1064
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6909 ATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATA 6850

Qy      1065 TTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATC 1124
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6849 TTCTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATC 6790

Qy      1125 ATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTT 1184
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6789 ATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTT 6730

Qy      1185 TAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAA 1244
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Db      6729 TAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAA 6670

Qy      1245 CAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC 1304
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6669 CAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC 6610

Qy      1305 ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGG 1364
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6609 ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGG 6550

Qy      1365 CCTCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTAT 1424
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6549 CCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTAT 6490

Qy      1425 GTAAGCAGACAGTTTTATTGTTCATGATGATATATTTTTATCTTGTGCAATGTAACATCA 1484
            ||||||||||||||||||||
Db      6489 GTAAGCAGACAGTTTTATTGT---------------------------------------- 6469

Qy      1485 GAGATTTTGAGACACAACGTGGCTTTCCCCCCCCCCCCTGCAGCGTTTCTTCCTTTTCCC 1544

Db      6468 ---------------------------------------------------------- 6469

Qy      1545 CACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAG 1604

Db      6468 ---------------------------------------------------------- 6469

Qy      1605 GCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTT 1664

Db      6468 ---------------------------------------------------------- 6469

Qy      1665 AATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAAC 1724
                                                  ||||||||||||||||||||
Db      6468 ----------------------------------------TCATGACCAAAATCCCTTAAC 6448

Qy      1725 GTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 1784
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6447 GTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 6388

Qy      1785 ATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGG 1844
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6387 ATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGG 6328

Qy      1845 TGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCA 1904
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      6327 TGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCA 6268

Qy      1905 GAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGA 1964
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      6267 GAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGA 6208

Qy      1965 ACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTG---GCTGCTG 2021
            |||||||||||||||||||||||||||||||||||||||||||||||||   |||||||
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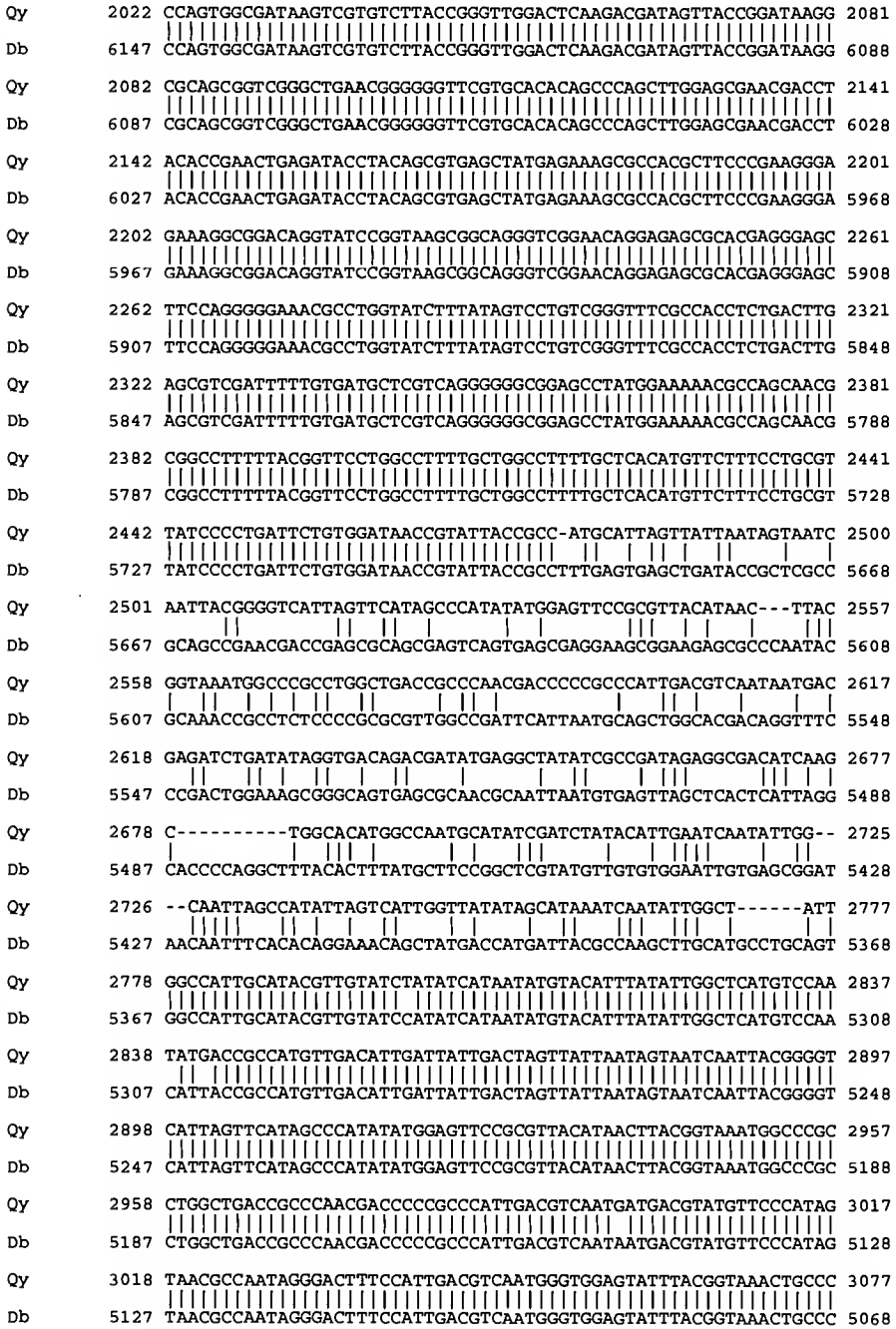
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Db 6147 CCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG 6088
Qy 2082 CGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT 2141
Db 6087 CGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCT 6028
Qy 2142 ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGA 2201
Db 6027 ACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGA 5968
Qy 2202 GAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGC 2261
Db 5967 GAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGC 5908
Qy 2262 TTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTG 2321
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Qy 2322 AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG 2381
Db 5847 AGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG 5788
Qy 2382 CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGT 2441
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Qy 2501 AATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAAC---TTAC 2557
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Qy 2558 GGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGAC 2617
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Qy 2618 GAGATCTGATATAGGTGACAGACGATATGAGGCTATATCGCCGATAGAGGCGACATCAAG 2677
Db 5547 CCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGG 5488
Qy 2678 C----------TGGCACATGGCCAATGCATATCGATCTATACATTGAATCAATATTGG-- 2725
Db 5487 CACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGAT 5428
Qy 2726 --CAATTAGCCATATTAGTCATTGGTTATATAGCATAAATCAATATTGGCT------ATT 2777
Db 5427 AACAATTTCACACAGGAAACAGCTATGACCATGATTACGCCAAGCTTGCATGCCTGCAGT 5368
Qy 2778 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2837
Db 5367 GGCCATTGCATACGTTGTATCCATATCATAATATGTACATTTATATTGGCTCATGTCCAA 5308
Qy 2838 TATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGT 2897
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Qy 2898 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2957
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Qy 2958 CTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATGATGACGTATGTTCCCATAG 3017
Db 5187 CTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG 5128
Qy 3018 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 3077
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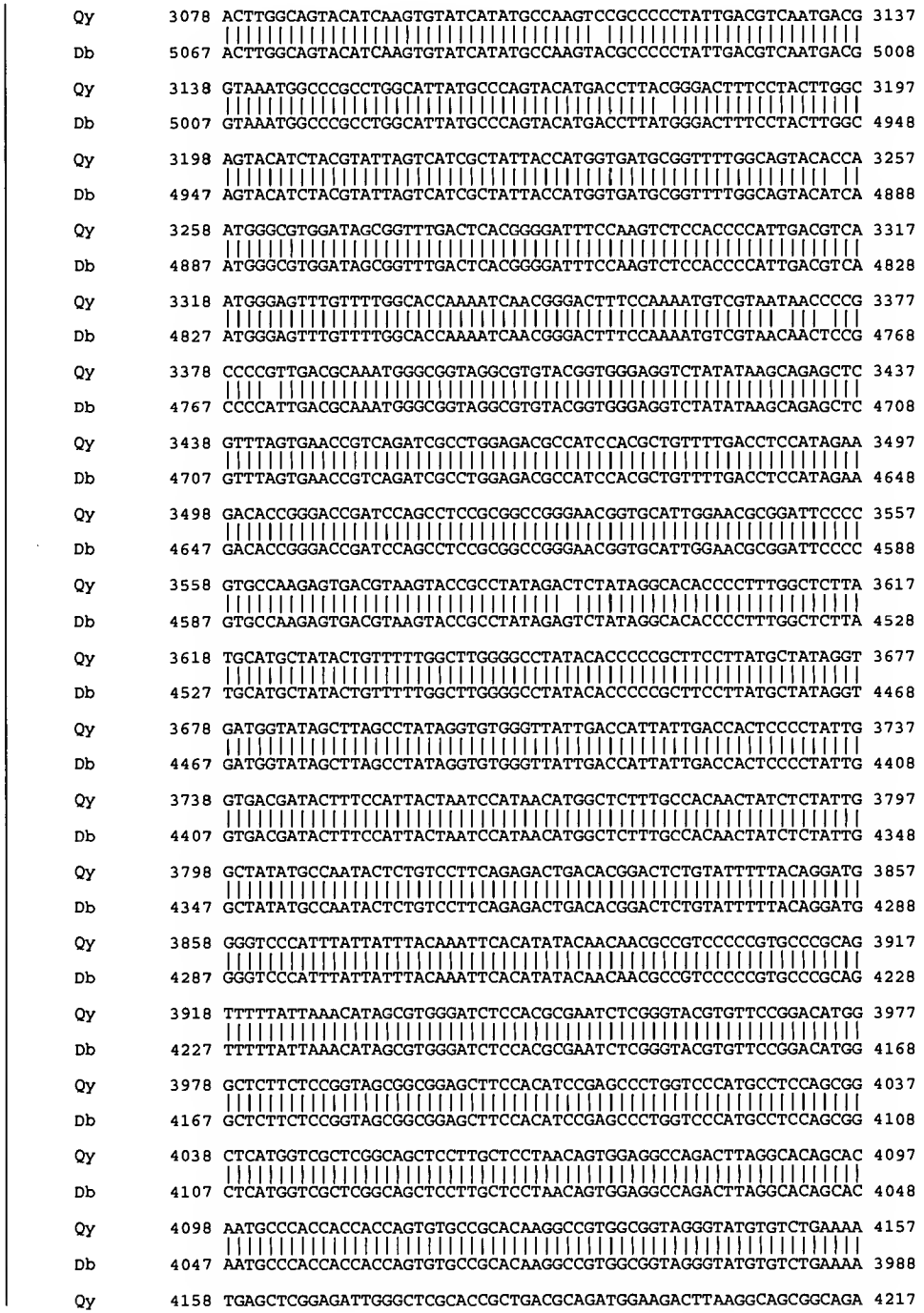
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Db 5007 GTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGC 4948
Qy 3198 AGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACCA 3257
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Qy 3318 ATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCCG 3377
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Qy 3378 CCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTC 3437
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Qy 3438 GTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAA 3497
Db 4707 GTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGAA 4648
Qy 3498 GACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCCC 3557
Db 4647 GACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCCC 4588
Qy 3558 GTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTTA 3617
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Qy 3618 TGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGGT 3677
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Qy 3738 GTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTG 3797
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Qy 3798 GCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGATG 3857
Db 4347 GCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGATG 4288
Qy 3858 GGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCAG 3917
Db 4287 GGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCAG 4228
Qy 3918 TTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGG 3977
Db 4227 TTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGG 4168
Qy 3978 GCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCGG 4037
Db 4167 GCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCGG 4108
Qy 4038 CTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCAC 4097
Db 4107 CTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCAC 4048
Qy 4098 AATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAAA 4157
Db 4047 AATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAAA 3988
Qy 4158 TGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAGA 4217

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                |||||  |||||||||||||||||  |||||||||||||||||||||||||||||||||||||
Db       3987 TGAGCGTGGAGATTGGGCTCGCACGGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAGA 3928

Qy       4218 AGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGC 4277
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3927 AGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGC 3868

Qy       4278 GGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCGCGC 4337
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3867 GGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCGC 3808

Qy       4338 CACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAG 4397
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3807 CACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAG 3748


RESULT 6
ABZ59287
ID   ABZ59287 standard; DNA; 5089 BP.
XX
AC   ABZ59287;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Plasmid pPJV2003 SEQ ID NO 2.
XX
KW   ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
KW   adjuvant; cholera toxin subunit B; CTB; human cytomegalovirus; hCMV;
KW   human tissue plasminogen activator; circular; cyclic; ds.
XX
OS   Synthetic.
XX
PN   WO2003004055-A2.
XX
PD   16-JAN-2003.
XX
PF   26-NOV-2001; 2001WO-US043151.
XX
PR   27-NOV-2000; 2000US-00724315.
XX
PA   (POWD-) POWDERJECT VACCINES INC.
XX
PI   Haynes JR,  Arrington JE;
XX
DR   WPI; 2003-221541/21.
XX
PT   New compositions comprising nucleic acid adjuvants, useful in
PT   immunization techniques, particularly for eliciting or enhancing an
PT   immune response against an antigen in a human.
XX
PS   Example 1; Fig 2; 143pp; English.
XX
CC   The invention relates to a composition comprising: (a) a first nucleic
CC   acid sequence that is a truncated A subunit coding region obtained or
CC   derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC   nucleic acid sequence that is a truncated B subunit coding region
CC   obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC   the truncated subunit coding regions has a 5' deletion and encodes a
CC   subunit peptide not having an amino terminal bacterial signal peptide.
CC   The composition is useful for eliciting an immune response against an
CC   antigen or for manufacturing a medicament for enhancing an immune
CC   response in a vertebrate subject (specifically a human) against an
CC   antigen. The composition is particularly useful as nucleic acid adjuvants
CC   for use in immunisation techniques. The present sequence is that of a
CC   plasmid expression vector that contains a truncated coding sequence for a
CC   cholera toxin (CT) subunit B (CTB) peptide, the human cytomegalovirus
CC   (hCMV) immediate early promoter and associated intron A sequence and the
CC   coding sequence for the signal peptide of human tissue plasminogen
CC   activator, to allow for secretion from mammalian cells of the truncated
CC   CTB expression product
XX
SQ   Sequence 5089 BP; 1268 A; 1260 C; 1267 G; 1294 T; 0 U; 0 Other;

  Query Match           37.1%;  Score 2378.8;  DB 7;  Length 5089;
  Best Local Similarity   91.6%;  Pred. No. 0;
. Matches 2598;  Conservative    0;  Mismatches  197;  Indels   41;  Gaps    6;

Qy       1615 AGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1674
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1675 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1127 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1186

Qy       1735 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1187 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1246

Qy       1795 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1247 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1306

Qy       1855 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1307 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1366

Qy       1915 ACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1974
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 ACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1426

Qy       1975 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 2034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1427 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 1486

Qy       2035 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 2094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1487 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 1546

Qy       2095 CTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 2154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1547 CTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 1606

Qy       2155 ATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 2214
              ||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||
Db       1607 ATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 1666

Qy       2215 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 2274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1667 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 1726

Qy       2275 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 2334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1727 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 1786

Qy       2335 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 2394
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 1846

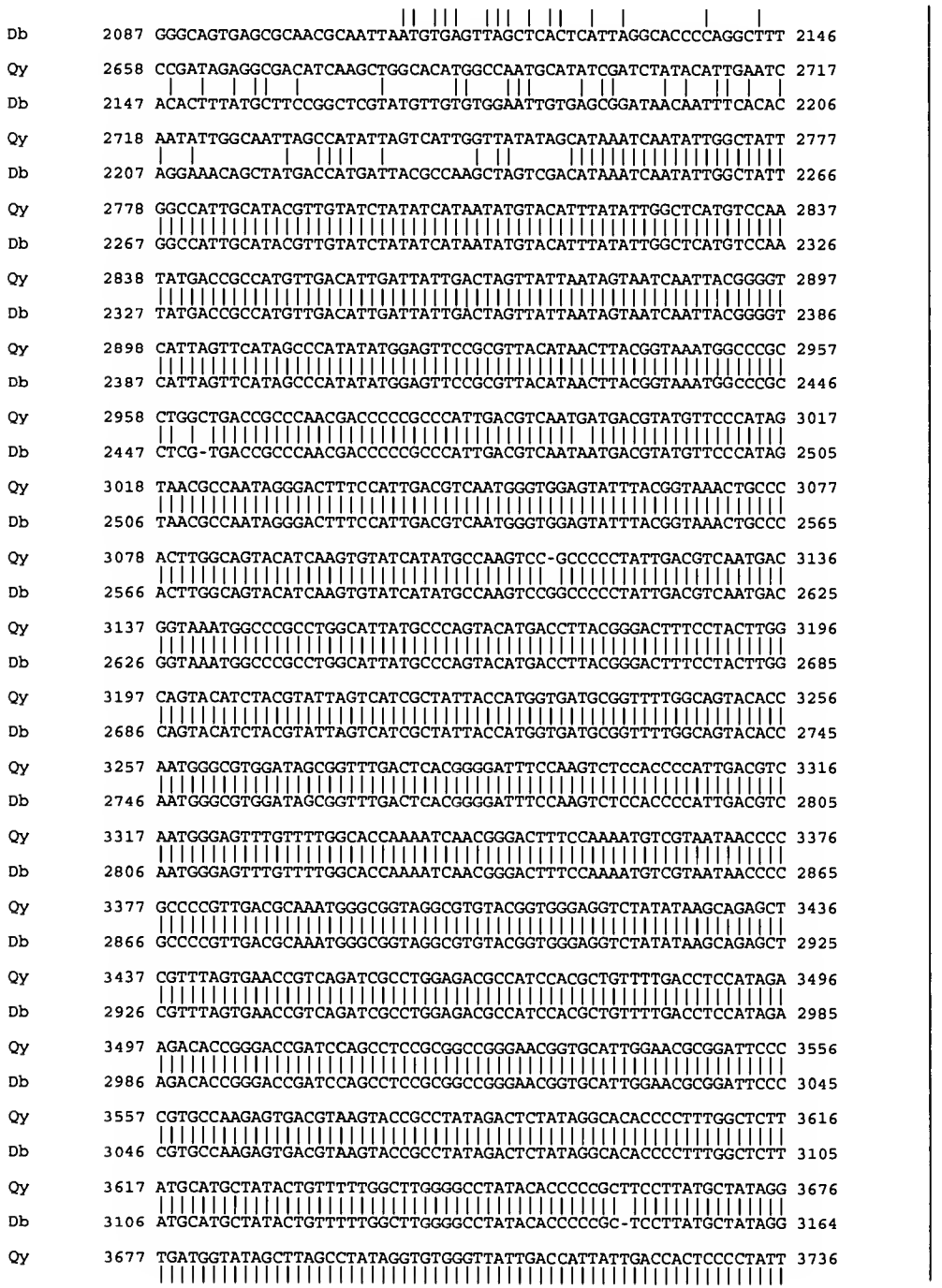
Qy       2395 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 2454
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1847 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 1906

Qy       2455 TGTGGATAACCGTATTACCGCCATGCATTAGTTATTAATAGTAATC---------AATTA 2505
              ||||||||||||||||||||  |  |  |  |  |  |  |  |         |    |
Db       1907 TGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGAC 1966

Qy       2506 CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG 2565
              ||| |  ||     |||  |  |  |  |  |  |||   |||   |    |
Db       1967 CGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCT 2026

Qy       2566 GCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGAG----- 2620
              |||||  |  | |   ||  | |        |||     |  |||  |
Db       2027 CCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGC 2086

Qy       2621 ----------------------ATCTGATATAGGTGACAGACGATATGAGGCTATATCG 2657
```



RESULT 7
ABZ59290
ID ABZ59290 standard; DNA; 5089 BP.
XX
AC ABZ59290;
XX
DT 10-MAY-2003 (first entry)
XX
DE Plasmid pPJV2005 SEQ ID NO 5.
XX
KW ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
KW adjuvant; labile enterotoxin subunit B; LTB; human cytomegalovirus; hCMV;
KW human tissue plasminogen activator; circular; cyclic; ds.
XX
OS Synthetic.
XX
PN WO2003004055-A2.
XX
PD 16-JAN-2003.
XX
PF 26-NOV-2001; 2001WO-US043151.
XX

PR 27-NOV-2000; 2000US-00724315.
XX
PA (POWD-) POWDERJECT VACCINES INC.
XX
PI Haynes JR, Arrington JE;
XX
DR WPI; 2003-221541/21.
XX
PT New compositions comprising nucleic acid adjuvants, useful in
PT immunization techniques, particularly for eliciting or enhancing an
PT immune response against an antigen in a human.
XX
PS Example 2; Fig 5; 143pp; English.
XX
CC The invention relates to a composition comprising: (a) a first nucleic
CC acid sequence that is a truncated A subunit coding region obtained or
CC derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC nucleic acid sequence that is a truncated B subunit coding region
CC obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC the truncated subunit coding regions has a 5' deletion and encodes a
CC subunit peptide not having an amino terminal bacterial signal peptide.
CC The composition is useful for eliciting an immune response against an
CC antigen or for manufacturing a medicament for enhancing an immune
CC response in a vertebrate subject (specifically a human) against an
CC antigen. The composition is particularly useful as nucleic acid adjuvants
CC for use in immunisation techniques. The present sequence is that of a
CC plasmid expression vector that contains a truncated coding sequence for
CC an E. coli heat labile enterotoxin (LT) subunit B (LTB) peptide, the
CC human cytomegalovirus (hCMV) immediate early promoter and associated
CC intron A sequence and the coding sequence for the signal peptide of human
CC tissue plasminogen activator, to allow for secretion from mammalian cells
CC of the truncated LTB expression product
XX
SQ Sequence 5089 BP; 1270 A; 1273 C; 1267 G; 1279 T; 0 U; 0 Other;

Query Match 37.1%; Score 2378.8; DB 7; Length 5089;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

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Qy    1615 AGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1674
           || |  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1067 AGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1126

Qy    1675 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1734
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1127 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1186

Qy    1735 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1794
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1187 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1246

Qy    1795 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1854
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1247 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1306

Qy    1855 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1914
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1307 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1366

Qy    1915 ACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1974
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1367 ACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1426

Qy    1975 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 2034
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1427 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 1486

Qy    2035 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 2094
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1487 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 1546

Qy    2095 CTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 2154
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    1547 CTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 1606

Qy    2155 ATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 2214
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    1607 ATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 1666

Qy    2215 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 2274
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1667 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 1726

Qy    2275 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 2334
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Db    1727 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 1786

Qy    2335 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 2394
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Db    1787 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 1846

Qy    2395 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 2454
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Db    1847 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 1906

Qy    2455 TGTGGATAACCGTATTACCGCCATGCATTAGTTATTAATAGTAATC---------AATTA 2505
           ||||||||||||||||||||| | | |  |  |  |  |  |         |
Db    1907 TGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGAC 1966

Qy    2506 CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG 2565
           || |  ||    |||  |  |  | |  |  |||   |||   |
Db    1967 CGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCT 2026

Qy    2566 GCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGAG----- 2620
           |||||  |  | |  ||  |  |    |||    |  |||  |
Db    2027 CCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGC 2086

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                                  || |||  ||| | ||  |  |  |    |  |
Db    2087 GGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTT 2146

Qy    2658 CCGATAGAGGCGACATCAAGCTGGCACATGGCCAATGCATATCGATCTATACATTGAATC 2717
           | |  | || |       |    ||  |||   | ||   | |  || | |
Db    2147 ACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACAC 2206

Qy    2718 AATATTGGCAATTAGCCATATTAGTCATTGGTTATATAGCATAAATCAATATTGGCTATT 2777
           | |    | ||||  |    | ||   |||||||||||||||||||
Db    2207 AGGAAACAGCTATGACCATGATTACGCCAAGCTAGTCGACATAAATCAATATTGGCTATT 2266

Qy    2778 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2837
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Db    2267 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2326

Qy    2838 TATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGT 2897
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Db    2327 TATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGT 2386

Qy    2898 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2957
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Db    2387 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2446

Qy    2958 CTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATGATGACGTATGTTCCCATAG 3017
           || | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2447 CTCG-TGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG 2505

Qy    3018 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 3077
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Db    2506 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 2565

Qy    3078 ACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCC-GCCCCCTATTGACGTCAATGAC 3136
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Db    2566 ACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGGCCCCCTATTGACGTCAATGAC 2625

Qy    3137 GGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGG 3196
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Qy       3197 CAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACC 3256
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Db       2686 CAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACC 2745

Qy       3257 AATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC 3316
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Db       2746 AATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC 2805

Qy       3317 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCC 3376
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Db       2806 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCC 2865

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Qy       3437 CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGA 3496
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Qy       3497 AGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCC 3556
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Qy       3677 TGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATT 3736
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Db       3165 TGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATT 3224

Qy       3737 GGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATT 3796
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Db       3225 GGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATT 3284

Qy       3797 GGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGAT 3856
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Db       3285 GGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGAT 3344

Qy       3857 GGGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCA 3916
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Qy       3917 GTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATG 3976
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3405 GTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATG 3464

Qy       3977 GGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCG 4036
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3465 GGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCG 3524

Qy       4037 GCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCA 4096
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Qy       4097 CAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAA 4156
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Db       3585 CAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAA 3644

Qy       4157 ATGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAG 4216
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Qy       4217 AAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTG 4276
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Db       3704 AAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTG 3763

Qy       4277 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 4336
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3764 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 3823

Qy       4337 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 4396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3824 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 3883

Qy       4397 GTCACCGTCCACGCGT 4412
             |||||||||||| || |
Db       3884 GTCACCGTCCAAGCTT 3899
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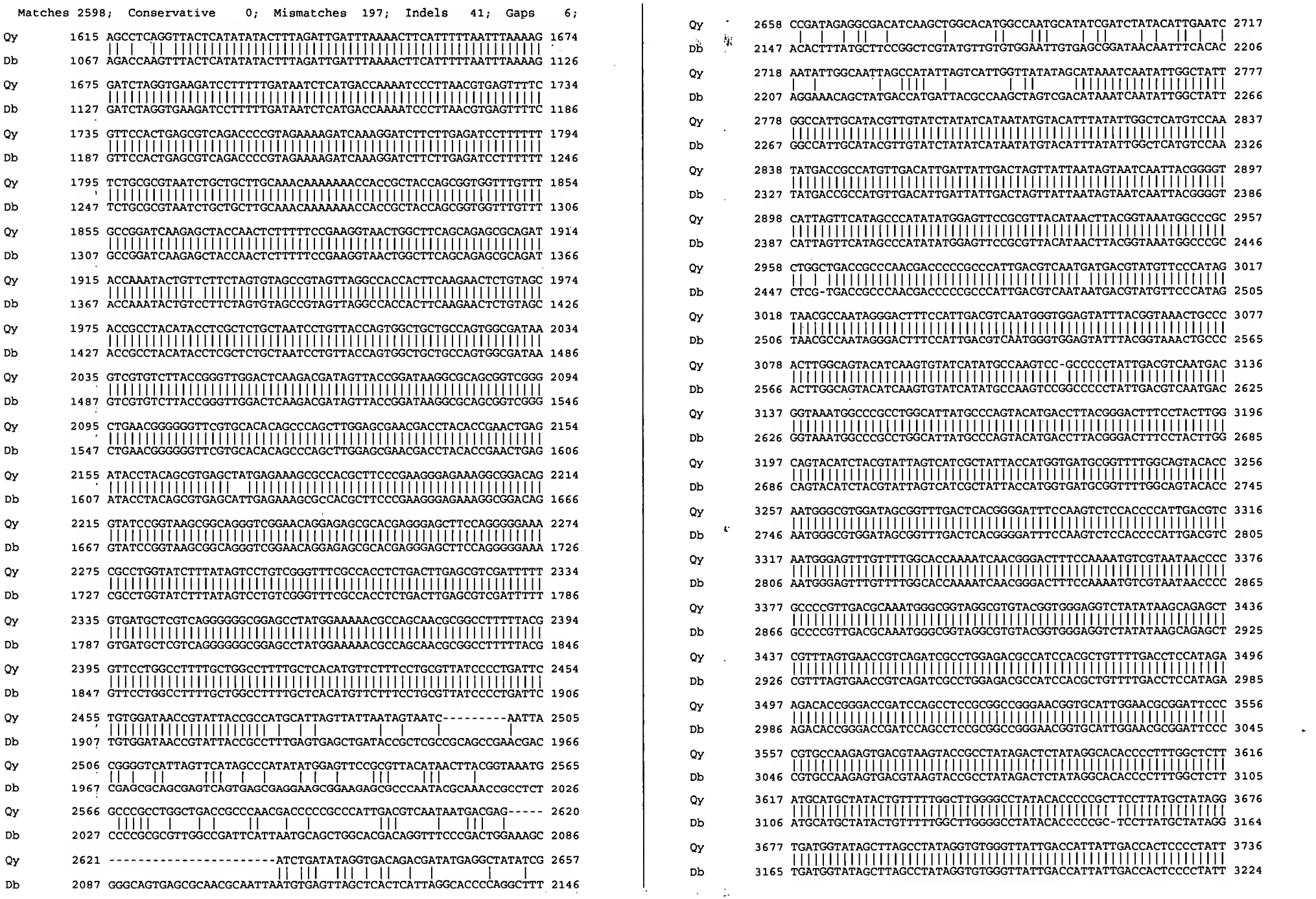
RESULT 8
ABZ59291
ID ABZ59291 standard; DNA; 5488 BP.
XX
AC ABZ59291;
XX
DT 10-MAY-2003 (first entry)
XX
DE Plasmid pPJV2006 SEQ ID NO 6.
XX
KW ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
KW adjuvant; labile enterotoxin subunit A; LTA; human cytomegalovirus; hCMV;
KW human tissue plasminogen activator; circular; cyclic; ds.
XX
OS Synthetic.
XX
PN WO2003004055-A2.
XX
PD 16-JAN-2003.
XX
PF 26-NOV-2001; 2001WO-US043151.
XX
PR 27-NOV-2000; 2000US-00724315.
XX
PA (POWD-) POWDERJECT VACCINES INC.
XX
PI Haynes JR, Arrington JE;
XX
DR WPI; 2003-221541/21.
XX
PT New compositions comprising nucleic acid adjuvants, useful in
PT immunization techniques, particularly for eliciting or enhancing an
PT immune response against an antigen in a human.
XX
PS Example 2; Fig 6; 143pp; English.
XX
CC The invention relates to a composition comprising: (a) a first nucleic
CC acid sequence that is a truncated A subunit coding region obtained or
CC derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC nucleic acid sequence that is a truncated B subunit coding region
CC obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC the truncated subunit coding regions has a 5' deletion and encodes a
CC subunit peptide not having an amino terminal bacterial signal peptide.
CC The composition is useful for eliciting an immune response against an
CC antigen or for manufacturing a medicament for enhancing an immune
CC response in a vertebrate subject (specifically a human) against an
CC antigen. The composition is particularly useful as nucleic acid adjuvants
CC for use in immunisation techniques. The present sequence is that of a
CC plasmid expression vector that contains a truncated coding sequence for
CC an E. coli heat labile enterotoxin (LT) subunit A (LTA) peptide with a
CC deletion of the C-terminal RDEL motif, the human cytomegalovirus (hCMV)
CC immediate early promoter and associated intron A sequence and the coding
CC sequence for the signal peptide of human tissue plasminogen activator, to
CC allow for secretion from mammalian cells of the truncated LTA expression
CC product
XX
SQ Sequence 5488 BP; 1381 A; 1339 C; 1362 G; 1406 T; 0 U; 0 Other;

Query Match 37.1%; Score 2378.8; DB 7; Length 5488;
Best Local Similarity 91.6%; Pred. No. 0;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Db 1067 AGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1126
Qy 1675 GATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1734
Db 1127 GATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1186
Qy 1735 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTT 1794
Db 1187 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTT 1246
Qy 1795 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1854
Db 1247 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1306
Qy 1855 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1914
Db 1307 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1366
Qy 1915 ACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1974
Db 1367 ACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1426
Qy 1975 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 2034
Db 1427 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 1486
Qy 2035 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 2094
Db 1487 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 1546
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Db 1607 ATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 1666
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Db 1667 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 1726
Qy 2275 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 2334
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Qy 2335 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 2394
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Qy 2395 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 2454
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Qy 2455 TGTGGATAACCGTATTACCGCCATGCATTAGTTATTAATAGTAATC---------AATTA 2505
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Qy 2506 CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG 2565
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Db 2027 CCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGC 2086
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Qy 2778 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2837
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Qy 2898 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2957
Db 2387 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2446
Qy 2958 CTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATGATGACGTATGTTCCCATAG 3017
Db 2447 CTCG-TGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG 2505
Qy 3018 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 3077
Db 2506 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 2565
Qy 3078 ACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCC-GCCCCCTATTGACGTCAATGAC 3136
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Qy 3137 GGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGG 3196
Db 2626 GGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGG 2685
Qy 3197 CAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACC 3256
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Qy 3317 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCC 3376
Db 2806 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCC 2865
Qy 3377 GCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT 3436
Db 2866 GCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT 2925
Qy 3437 CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGA 3496
Db 2926 CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGA 2985
Qy 3497 AGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCC 3556
Db 2986 AGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCC 3045
Qy 3557 CGTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTT 3616
Db 3046 CGTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTT 3105
Qy 3617 ATGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGG 3676
Db 3106 ATGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCCGC-TCCTTATGCTATAGG 3164
Qy 3677 TGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATT 3736
Db 3165 TGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATT 3224

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Qy       3737 GGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATT 3796
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Db       3225 GGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATT 3284

Qy       3797 GGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGAT 3856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3285 GGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGAT 3344

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Qy       4037 GCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCA 4096
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Db       3525 GCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCA 3584

Qy       4097 CAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAA 4156
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Db       3585 CAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAA 3644

Qy       4157 ATGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAG 4216
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
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Qy       4217 AAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTG 4276
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3704 AAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTG 3763

Qy       4277 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 4336
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Db       3764 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 3823

Qy       4337 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 4396
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3824 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 3883

Qy       4397 GTCACCGTCCACGCGT 4412
             |||||||||| || |
Db       3884 GTCACCGTCCAAGCTT 3899
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RESULT 9
ABZ59288
ID ABZ59288 standard; DNA; 5488 BP.
XX
AC ABZ59288;
XX
DT 10-MAY-2003 (first entry)
XX
DE Plasmid pPJV2006 SEQ ID NO 3.
XX
KW ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
KW adjuvant; cholera toxin subunit A; CTA; human cytomegalovirus; hCMV;
KW human tissue plasminogen activator; circular; cyclic; ds.
XX
OS Synthetic.
XX
PN WO2003004055-A2.
XX
PD 16-JAN-2003.
XX
PF 26-NOV-2001; 2001WO-US043151.
XX
PR 27-NOV-2000; 2000US-00724315.
XX
PA (POWD-) POWDERJECT VACCINES INC.
XX
PI Haynes JR, Arrington JE;
XX
DR WPI; 2003-221541/21.
XX
PT New compositions comprising nucleic acid adjuvants, useful in
PT immunization techniques, particularly for eliciting or enhancing an
PT immune response against an antigen in a human.
XX
PS Example 1; Fig 3; 143pp; English.
XX
CC The invention relates to a composition comprising: (a) a first nucleic
CC acid sequence that is a truncated A subunit coding region obtained or
CC derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC nucleic acid sequence that is a truncated B subunit coding region
CC obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC the truncated subunit coding regions has a 5' deletion and encodes a
CC subunit peptide not having an amino terminal bacterial signal peptide.
CC The composition is useful for eliciting an immune response against an
CC antigen or for manufacturing a medicament for enhancing an immune
CC response in a vertebrate subject (specifically a human) against an
CC antigen. The composition is particularly useful as nucleic acid adjuvants
CC for use in immunisation techniques. The present sequence is that of a
CC plasmid expression vector that contains a truncated coding sequence for a
CC cholera toxin (CT) subunit A (CTA) peptide with an addition deletion at
CC the C-terminal KDEL motif, the human cytomegalovirus (hCMV) immediate
CC early promoter and associated intron A sequence and the coding sequence
CC for the signal peptide of human tissue plasminogen activator, to allow
CC for secretion from mammalian cells of the truncated CTA expression
CC product
XX
SQ Sequence 5488 BP; 1367 A; 1336 C; 1370 G; 1415 T; 0 U; 0 Other;

Query Match 37.1%; Score 2378.8; DB 7; Length 5488;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

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Db       1067 AGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1126

Qy       1675 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1734
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Db       1127 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1186

Qy       1735 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1794
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Db       1187 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1246

Qy       1795 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1854
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Db       1247 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1306

Qy       1855 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1914
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Db       1307 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1366

Qy       1915 ACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1974
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 ACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1426

Qy       1975 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 2034
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Db       1427 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 1486

Qy       2035 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 2094
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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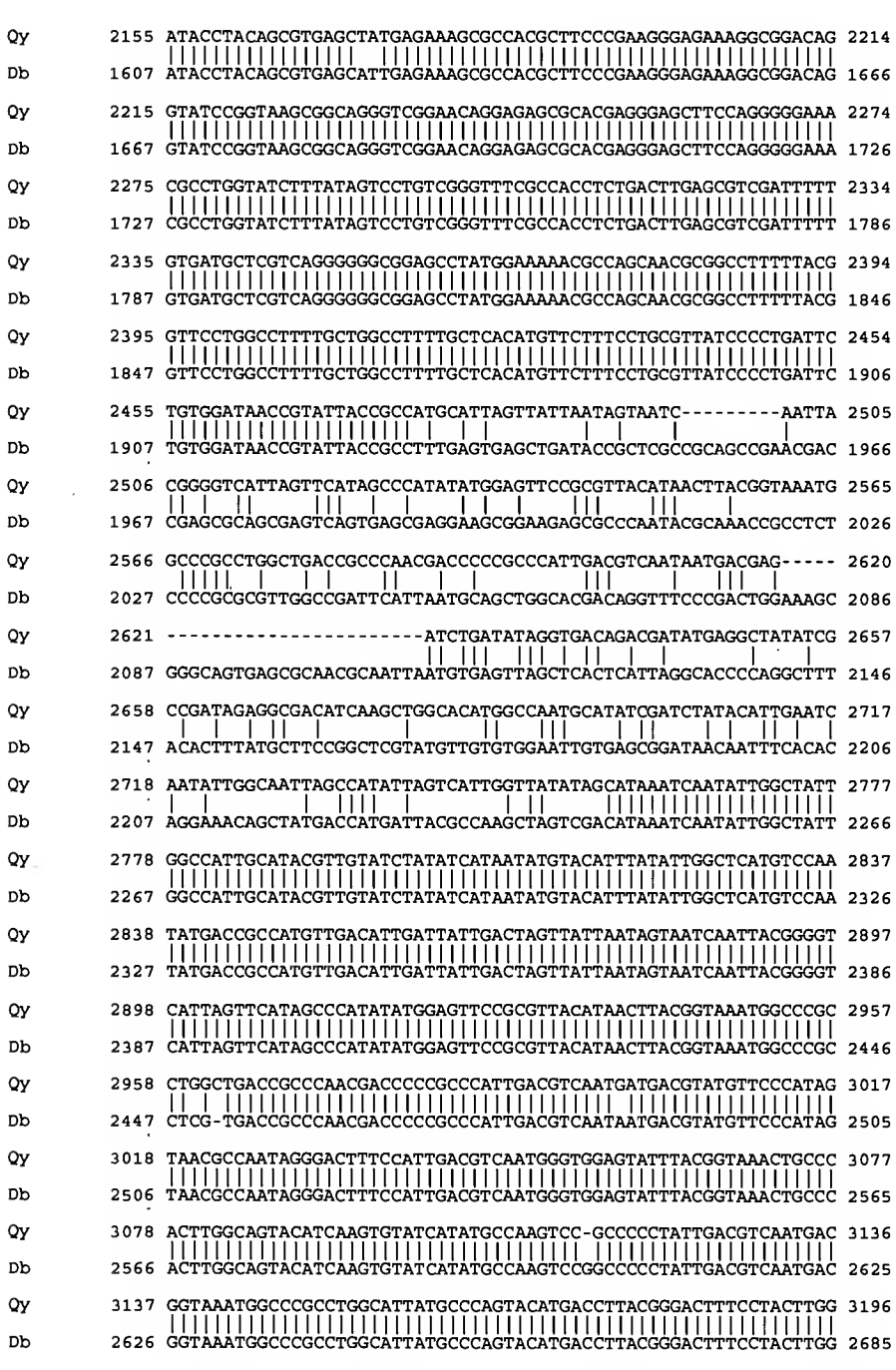

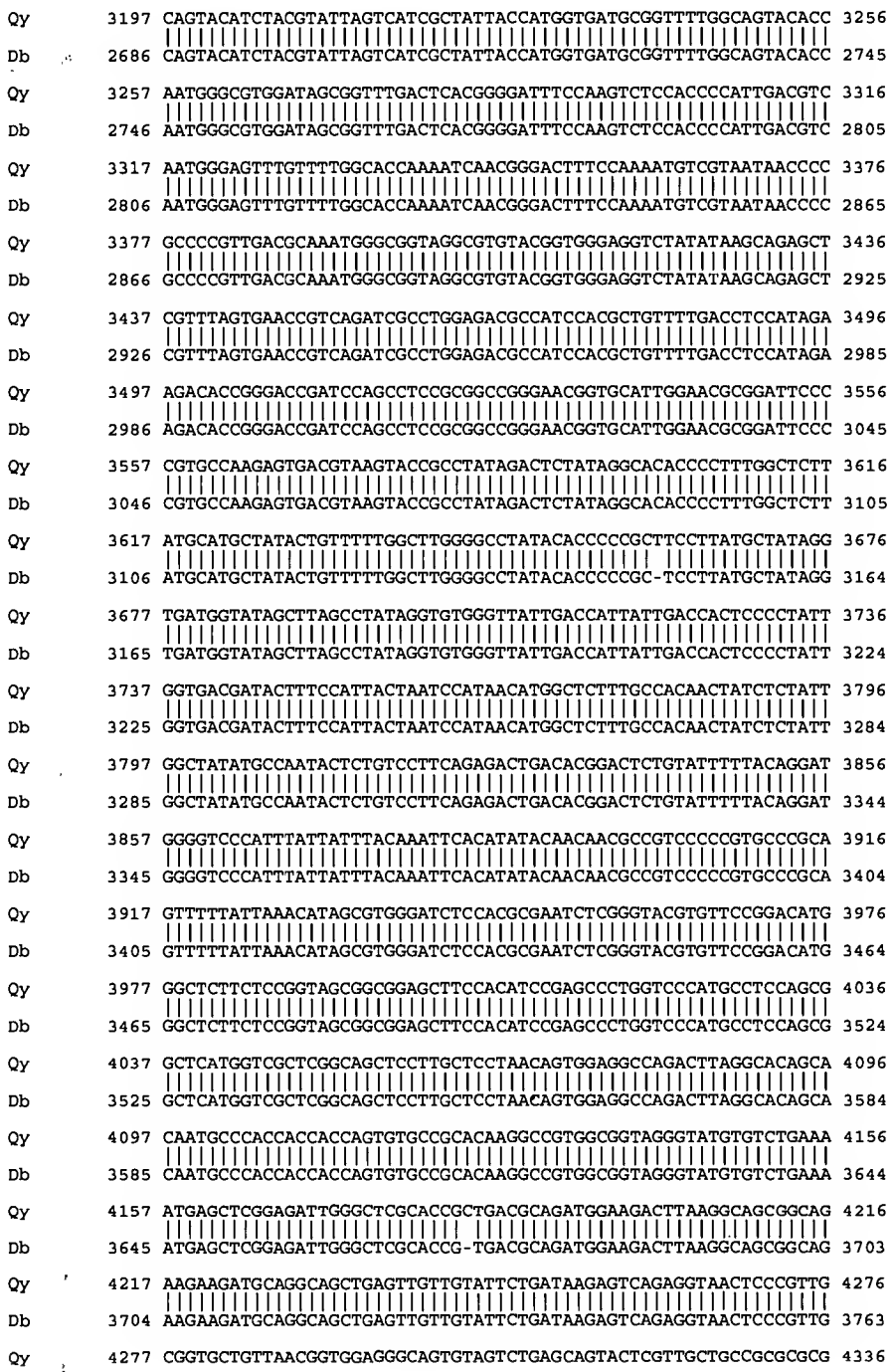

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Db        3764 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 3823

Qy        4337 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 4396
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3824 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 3883

Qy        4397 GTCACCGTCCACGCGT 4412
               |||||||||| || |
Db        3884 GTCACCGTCCAAGCTT 3899
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RESULT 10
ABZ59289
ID   ABZ59289 standard; DNA; 5500 BP.
XX
AC   ABZ59289;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Plasmid pPJV2004 SEQ ID NO 4.
XX
KW   ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
KW   adjuvant; labile enterotoxin subunit A; LTA; human cytomegalovirus; hCMV;
KW   human tissue plasminogen activator; circular; cyclic; ds.
XX
OS   Synthetic.
XX
PN   WO2003004055-A2.
XX
PD   16-JAN-2003.
XX
PF   26-NOV-2001; 2001WO-US043151.
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PR   27-NOV-2000; 2000US-00724315.
XX
PA   (POWD-) POWDERJECT VACCINES INC.
XX
PI   Haynes JR,  Arrington JE;
XX
DR   WPI; 2003-221541/21.
XX
PT   New compositions comprising nucleic acid adjuvants, useful in
PT   immunization techniques, particularly for eliciting or enhancing an
PT   immune response against an antigen in a human.
XX
PS   Example 2; Fig 4; 143pp; English.
XX
CC   The invention relates to a composition comprising: (a) a first nucleic
CC   acid sequence that is a truncated A subunit coding region obtained or
CC   derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC   nucleic acid sequence that is a truncated B subunit coding region
CC   obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC   the truncated subunit coding regions has a 5' deletion and encodes a
CC   subunit peptide not having an amino terminal bacterial signal peptide.
CC   The composition is useful for eliciting an immune response against an
CC   antigen or for manufacturing a medicament for enhancing an immune
CC   response in a vertebrate subject (specifically a human) against an
CC   antigen. The composition is particularly useful as nucleic acid adjuvants
CC   for use in immunisation techniques. The present sequence is that of a
CC   plasmid expression vector that contains a truncated coding sequence for
CC   an E. coli heat labile enterotoxin (LT) subunit A (LTA) peptide, the
CC   human cytomegalovirus (hCMV) immediate early promoter and associated
CC   intron A sequence and the coding sequence for the signal peptide of human
CC   tissue plasminogen activator, to allow for secretion from mammalian cells
CC   of the truncated LTA expression product
XX
SQ   Sequence 5500 BP; 1385 A; 1340 C; 1367 G; 1408 T; 0 U; 0 Other;

  Query Match             37.1%;  Score 2378.8;  DB 7;  Length 5500;
  Best Local Similarity   91.6%;  Pred. No. 0;
  Matches 2598;  Conservative    0;  Mismatches  197;  Indels   41;  Gaps    6;
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Qy        1615 AGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1674
               || |  ||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1067 AGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1126

Qy        1675 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1734
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1127 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1186

Qy        1735 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1794
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1187 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1246

Qy        1795 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1854
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1247 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1306

Qy        1855 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1914
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Db        1307 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1366

Qy        1915 ACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1974
               |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        1367 ACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1426

Qy        1975 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 2034
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Qy        2095 CTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 2154
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Db        1547 CTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 1606

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Db        1607 ATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 1666

Qy        2215 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 2274
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Db        1667 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 1726

Qy        2275 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 2334
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Qy        2335 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 2394
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1787 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 1846

Qy        2395 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 2454
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1847 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 1906

Qy        2455 TGTGGATAACCGTATTACCGCCATGCATTAGTTATTAATAGTAATC---------AATTA 2505
               |||||||||||||||||||||| |  |       |  |   |          |
Db        1907 TGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGAC 1966

Qy        2506 CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG 2565
               || |  ||     |||  |  |    | |  |    |||     |||     |
Db        1967 CGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCT 2026

Qy        2566 GCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGAG----- 2620
                |||||  |   | |   ||   |  |          |||     |    |||  |
Db        2027 CCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGC 2086

Qy        2621 ----------------------ATCTGATATAGGTGACAGACGATATGAGGCTATATCG 2657
                                     || |||  ||| | ||  |  |       |   |
Db        2087 GGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTT 2146

Qy        2658 CCGATAGAGGCGACATCAAGCTGGCACATGGCCAATGCATATCGATCTATACATTGAATC 2717
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Db       2147 ACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACAC 2206
Qy       2718 AATATTGGCAATTAGCCATATTAGTCATTGGTTATATAGCATAAATCAATATTGGCTATT 2777
Db       2207 AGGAAACAGCTATGACCATGATTACGCCAAGCTAGTCGACATAAATCAATATTGGCTATT 2266
Qy       2778 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2837
Db       2267 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2326
Qy       2838 TATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGT 2897
Db       2327 TATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGT 2386
Qy       2898 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2957
Db       2387 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2446
Qy       2958 CTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATGATGACGTATGTTCCCATAG 3017
Db       2447 CTCG-TGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG 2505
Qy       3018 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 3077
Db       2506 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 2565
Qy       3078 ACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCC-GCCCCCTATTGACGTCAATGAC 3136
Db       2566 ACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGGCCCCCTATTGACGTCAATGAC 2625
Qy       3137 GGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGG 3196
Db       2626 GGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGG 2685
Qy       3197 CAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACC 3256
Db       2686 CAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACC 2745
Qy       3257 AATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC 3316
Db       2746 AATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC 2805
Qy       3317 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCC 3376
Db       2806 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCC 2865
Qy       3377 GCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT 3436
Db       2866 GCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT 2925
Qy       3437 CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGA 3496
Db       2926 CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGA 2985
Qy       3497 AGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCC 3556
Db       2986 AGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCC 3045
Qy       3557 CGTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTT 3616
Db       3046 CGTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTT 3105
Qy       3617 ATGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGG 3676
Db       3106 ATGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCCGC-TCCTTATGCTATAGG 3164
Qy       3677 TGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATT 3736
Db       3165 TGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATT 3224
Qy       3737 GGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATT 3796
Db       3225 GGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATT 3284
Qy       3797 GGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGAT 3856
Db       3285 GGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGAT 3344
Qy       3857 GGGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCA 3916
Db       3345 GGGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCA 3404
Qy       3917 GTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATG 3976
Db       3405 GTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATG 3464
Qy       3977 GGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCG 4036
Db       3465 GGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCG 3524
Qy       4037 GCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCA 4096
Db       3525 GCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCA 3584
Qy       4097 CAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAA 4156
Db       3585 CAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAA 3644
Qy       4157 ATGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAG 4216
Db       3645 ATGAGCTCGGAGATTGGGCTCGCACCG-TGACGCAGATGGAAGACTTAAGGCAGCGGCAG 3703
Qy       4217 AAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTG 4276
Db       3704 AAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTG 3763
Qy       4277 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 4336
Db       3764 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 3823
Qy       4337 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 4396
Db       3824 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 3883
Qy       4397 GTCACCGTCCACGCGT 4412
Db       3884 GTCACCGTCCAAGCTT 3899
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RESULT 11
ABZ59286
ID ABZ59286 standard; DNA; 5500 BP.
XX
AC ABZ59286;
XX
DT 10-MAY-2003 (first entry)
XX
DE Plasmid pPJV2002 SEQ ID NO 1.
XX
KW ADP-ribosylating exotoxin; immune response; immunisation; vaccine;
KW adjuvant; cholera toxin subunit A; CTA; human cytomegalovirus; hCMV;
KW human tissue plasminogen activator; circular; cyclic; ds.
XX
OS Synthetic.
XX
PN WO2003004055-A2.
XX
PD 16-JAN-2003.
XX
PF 26-NOV-2001; 2001WO-US043151.
XX
PR 27-NOV-2000; 2000US-00724315.
XX
PA (POWD-) POWDERJECT VACCINES INC.
XX

PI Haynes JR, Arrington JE;
XX
DR WPI; 2003-221541/21.
XX
PT New compositions comprising nucleic acid adjuvants, useful in
PT immunization techniques, particularly for eliciting or enhancing an
PT immune response against an antigen in a human.
XX
PS Example 1; Fig 1; 143pp; English.
XX
CC The invention relates to a composition comprising: (a) a first nucleic
CC acid sequence that is a truncated A subunit coding region obtained or
CC derived from a bacterial ADP-ribosylating exotoxin; and (b) a second
CC nucleic acid sequence that is a truncated B subunit coding region
CC obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of
CC the truncated subunit coding regions has a 5' deletion and encodes a
CC subunit peptide not having an amino terminal bacterial signal peptide.
CC The composition is useful for eliciting an immune response against an
CC antigen or for manufacturing a medicament for enhancing an immune
CC response in a vertebrate subject (specifically a human) against an
CC antigen. The composition is particularly useful as nucleic acid adjuvants
CC for use in immunisation techniques. The present sequence is that of a
CC plasmid expression vector that contains a truncated coding sequence for a
CC cholera toxin (CT) subunit A (CTA) peptide, the human cytomegalovirus
CC (hCMV) immediate early promoter and associated intron A sequence and the
CC coding sequence for the signal peptide of human tissue plasminogen
CC activator, to allow for secretion from mammalian cells of the truncated
CC CTA expression product
XX
SQ Sequence 5500 BP; 1373 A; 1336 C; 1373 G; 1418 T; 0 U; 0 Other;

Query Match 37.1%; Score 2378.8; DB 7; Length 5500;
Best Local Similarity 91.6%; Pred. No. 0;
Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

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Qy       1615 AGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1674
             || |  || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1067 AGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1126

Qy       1675 GATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1734
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1127 GATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1186

Qy       1735 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1794
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1187 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1246

Qy       1795 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1854
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1247 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1306

Qy       1855 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1914
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1307 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1366

Qy       1915 ACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1974
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1367 ACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1426

Qy       1975 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 2034
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1427 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 1486

Qy       2035 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 2094
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1487 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 1546

Qy       2095 CTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 2154
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1547 CTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 1606

Qy       2155 ATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 2214
             ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db       1607 ATACCTACAGCGTGAGCATTGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 1666

Qy       2215 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 2274
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1667 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 1726

Qy       2275 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 2334
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1727 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 1786

Qy       2335 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 2394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1787 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 1846

Qy       2395 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 2454
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1847 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 1906

Qy       2455 TGTGGATAACCGTATTACCGCCATGCATTAGTTATTAATAGTAATC---------AATTA 2505
             ||||||||||||||||||||| | | |         | |   |   |         |
Db       1907 TGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGAC 1966

Qy       2506 CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG 2565
             || |  ||     ||| |  |     | |  |    |||    |||    |
Db       1967 CGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAACCGCCTCT 2026

Qy       2566 GCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGAG----- 2620
              ||||| |  | |   ||  | |         |||    |   |||  |
Db       2027 CCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGC 2086

Qy       2621 ----------------------ATCTGATATAGGTGACAGACGATATGAGGCTATATCG 2657
                                   || ||| ||| | ||  |  |     |   |
Db       2087 GGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTT 2146

Qy       2658 CCGATAGAGGCGACATCAAGCTGGCACATGGCCAATGCATATCGATCTATACATTGAATC 2717
              |  |  | ||  |       |    ||   |||    | ||    | |  || |  |
Db       2147 ACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTCACAC 2206

Qy       2718 AATATTGGCAATTAGCCATATTAGTCATTGGTTATATAGCATAAATCAATATTGGCTATT 2777
              |  |         |  ||||  |       | ||     ||||||||||||||||||
Db       2207 AGGAAACAGCTATGACCATGATTACGCCAAGCTAGTCGACATAAATCAATATTGGCTATT 2266

Qy       2778 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2837
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2267 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2326

Qy       2838 TATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGT 2897
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2327 TATGACCGCCATGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGT 2386

Qy       2898 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2957
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2387 CATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGC 2446

Qy       2958 CTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATGATGACGTATGTTCCCATAG 3017
              || | ||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       2447 CTCG-TGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG 2505

Qy       3018 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 3077
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2506 TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCC 2565

Qy       3078 ACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCC-GCCCCCTATTGACGTCAATGAC 3136
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db       2566 ACTTGGCAGTACATCAAGTGTATCATATGCCAAGTCCGGCCCCCTATTGACGTCAATGAC 2625

Qy       3137 GGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGG 3196
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 GGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGG 2685

Qy       3197 CAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACC 3256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2686 CAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACACC 2745
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Qy       3257 AATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC 3316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2746 AATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC 2805

Qy       3317 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCC 3376
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Db       2806 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAATAACCCC 2865

Qy       3377 GCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT 3436
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2866 GCCCCGTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT 2925

Qy       3437 CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGA 3496
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2926 CGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGACCTCCATAGA 2985

Qy       3497 AGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCC 3556
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2986 AGACACCGGGACCGATCCAGCCTCCGCGGCCGGGAACGGTGCATTGGAACGCGGATTCCC 3045

Qy       3557 CGTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTT 3616
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3046 CGTGCCAAGAGTGACGTAAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTT 3105

Qy       3617 ATGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCGCTTCCTTATGCTATAGG 3676
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       3106 ATGCATGCTATACTGTTTTTGGCTTGGGGCCTATACACCCCGC-TCCTTATGCTATAGG 3164

Qy       3677 TGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATT 3736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3165 TGATGGTATAGCTTAGCCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATT 3224

Qy       3737 GGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATT 3796
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Db       3225 GGTGACGATACTTTCCATTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATT 3284

Qy       3797 GGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGAT 3856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3285 GGCTATATGCCAATACTCTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGAT 3344

Qy       3857 GGGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCA 3916
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3345 GGGGTCCCATTTATTATTTACAAATTCACATATACAACAACGCCGTCCCCCGTGCCCGCA 3404

Qy       3917 GTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATG 3976
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3405 GTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATG 3464

Qy       3977 GGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCG 4036
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3465 GGCTCTTCTCCGGTAGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCG 3524

Qy       4037 GCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCA 4096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3525 GCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCA 3584

Qy       4097 CAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAA 4156
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3585 CAATGCCCACCACCACCAGTGTGCCGCACAAGGCCGTGGCGGTAGGGTATGTGTCTGAAA 3644

Qy       4157 ATGAGCTCGGAGATTGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAG 4216
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db       3645 ATGAGCTCGGAGATTGGGCTCGCACCG-TGACGCAGATGGAAGACTTAAGGCAGCGGCAG 3703

Qy       4217 AAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTG 4276
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3704 AAGAAGATGCAGGCAGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTG 3763

Qy       4277 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 4336
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Db       3764 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 3823

Qy       4337 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 4396
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Db       3824 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 3883

Qy       4397 GTCACCGTCCACGCGT 4412
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Db       3884 GTCACCGTCCAAGCTT 3899
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RESULT 12
ADE06467
ID ADE06467 standard; DNA; 10466 BP.
XX
AC ADE06467;
XX
DT 29-JAN-2004 (first entry)
XX
DE Vector pGA1/IN2.
XX
KW HIV infection; Anti-HIV; vaccine; ds.
XX
OS Synthetic.
XX

FH	Key	Location/Qualifiers
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FT		finger packaging sequences for viral RNA"
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FT		/*tag= b
FT		/product= "Pol, with inactivating point mutations in
FT		reverse transcriptase, deletion of integrase"
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XX
PN WO2003076591-A2.
XX
PD 18-SEP-2003.
XX
PF 10-MAR-2003; 2003WO-US007177.
XX
PR 08-MAR-2002; 2002US-00093953.
PR 03-JAN-2003; 2003US-00336566.
XX
PA (UYEM-) UNIV EMORY.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Robinson HL, Smith J, Hua J, Moss B;
XX
DR WPI; 2003-731822/69.
XX
PT A composition for generating an immune response against HIV comprises a
PT vector comprising a vaccine insert encoding one or more antigens that
PT elicit an immune response against HIV.
XX
PS Example 16; Fig 18; 133pp; English.
XX

```
CC   The present invention relates to a composition comprising a first vector
CC   with a vaccine insert encoding one or more antigens that elicit an immune
CC   response against HIV or a first subtype or recombinant form; and a second
CC   vector comprising a vaccine insert encoding one or more antigens that
CC   elicit an immune response against an HIV of a second subtype or
CC   recombinant form. The composition is useful in generating an immune
CC   response against HIV. The insert of the first vector or the insert of the
CC   second vector comprises the sequences of two or more of: a gag, pol, env,
CC   tat, rev, nef, vif, vpr or vpu gene; or their mutants, and optionally;
CC   non-coding regulatory sequences of the HIV genome. At least one of the
CC   two or more sequences comprises mutations that limit the encapsidation of
CC   viral RNA, or a gag sequence having a mutation in one or more of the
CC   sequences encoding a zinc finger. All or part of cis-acting RNA
CC   encapsidation sequences have been deleted from the non-coding regulatory
CC   sequences of HIV-1. The two or more sequences comprise a pol sequence
CC   having a mutation that inhibits one or more of the enzymatic activities
CC   of pol. The enzymatic activity is integrase activity, reverse
CC   transcriptase activity or protease activity. The enzymatic activity is
CC   inhibited by deleting a portion of the pol sequence or introducing one or
CC   more point mutations into the pol sequence. The present sequence is one
CC   such vector used to illustrate the invention.
XX
SQ   Sequence 10466 BP; 3317 A; 2200 C; 2543 G; 2405 T; 0 U; 1 Other;

  Query Match            31.6%;  Score 2027.6;  DB 9;  Length 10466;
  Best Local Similarity  87.4%;  Pred. No. 0;
  Matches 2407;  Conservative    1;  Mismatches   15;  Indels  331;  Gaps    4;

Qy       1654 ACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAA 1713
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Qy       1834 GCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAC 1893
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Db       8221 GCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAC 8280

Qy       1894 TGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCA 1953
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Db       8281 TGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCA 8340

Qy       1954 CCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGT 2013
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Db       8341 CCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGT 8400

Qy       2014 GGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACC 2073
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Db       8401 GGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACC 8460

Qy       2074 GGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCG 2133
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Qy       2134 AACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC 2193
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Qy       2194 CGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCAC 2253
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Db       8581 CGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCAC 8640

Qy       2254 GAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCT 2313
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Db       8820 ------------------------------------------------------------ 8819

Qy       2494 AGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAAC 2553
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Qy       2554 TTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAA 2613
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Db       8820 ------------------------------------------------------------ 8819

Qy       2614 TGACGAGATCTGATATAGGTGACAGACGATATGAGGCTATATCGCCGATAGAGGCGACAT 2673
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Qy       2674 CAAGCTGGCACATGGCCAATGCATATCGATCTATACATTGAATCAATATTGGCAATTAGC 2733
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Qy       2734 CATATTAGTCATTGGTTATATAGCATAAATCAATATTGGCTATTGGCCATTGCATACGTT 2793
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Qy       2794 GTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAATATGACCGCCATGTTG 2853
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Qy       2854 ACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCC 2913
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Qy       2914 ATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAA 2973
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Qy       2974 CGACCCCCGCCCATTGACGTCAATGATGACGTATGTTCCCATAGTAACGCCAATAGGGAC 3033
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Qy       3154 GCATTATGCCCAGTACATGACCTTACGGGACTTTCCTACTTGGCAGTACATCTAC-GTAT 3212
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Qy       3991 AGCGGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCGGCTCATGGTCGCTC 4050
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Qy       4051 GGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCACAATGCCCACCACC 4110
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Db      10233 TGGGCTCGCACCGCTGACGCAGATGGAAGACTTAAGGCAGCGGCAGAAGAAGATGCAGGC 10292

Qy       4231 AGCTGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGCGGTGCTGTTAACG 4290
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Qy       4291 GTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCGCCACCAGACATAAT 4350
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Qy       4351 AGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAGTCACCGT 4404
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Db      10413 AGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAGTCACCAT 10466


RESULT 13
ADE06466
ID   ADE06466 standard; DNA; 10466 BP.
XX
AC   ADE06466;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Vector pGA1/IN3.
XX
KW   HIV infection; Anti-HIV; vaccine; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             99. .1577
FT                   /*tag=  a
FT                   /product= "Gag, with inactivating point mutations in zinc
FT                   finger packaging sequences for viral RNA"
FT   CDS             1382. .3520
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FT                   /product= "Pol, with inactivating point mutations in
FT                   reverse transcriptase, deletion of integrase"
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PN   WO2003076591-A2.
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PD   18-SEP-2003.
XX
PF   10-MAR-2003; 2003WO-US007177.
XX
PR   08-MAR-2002; 2002US-00093953.
PR   03-JAN-2003; 2003US-00336566.
XX
PA   (UYEM-) UNIV EMORY.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Robinson HL,  Smith J,  Hua J,  Moss B;
XX
DR   WPI; 2003-731822/69.
XX
PT   A composition for generating an immune response against HIV comprises a
PT   vector comprising a vaccine insert encoding one or more antigens that
PT   elicit an immune response against HIV.
XX
PS   Example 15; Fig 17; 133pp; English.
XX
CC   The present invention relates to a composition comprising a first vector
CC   with a vaccine insert encoding one or more antigens that elicit an immune
CC   response against HIV or a first subtype or recombinant form; and a second
CC   vector comprising a vaccine insert encoding one or more antigens that
CC   elicit an immune response against an HIV of a second subtype or
CC   recombinant form. The composition is useful in generating an immune
CC   response against HIV. The insert of the first vector or the insert of the
CC   second vector comprises the sequences of two or more of: a gag, pol, env,
CC   tat, rev, nef, vif, vpr or vpu gene; or their mutants, and optionally;
CC   non-coding regulatory sequences of the HIV genome. At least one of the
CC   two or more sequences comprises mutations that limit the encapsidation of
CC   viral RNA, or a gag sequence having a mutation in one or more of the
CC   sequences encoding a zinc finger. All or part of cis-acting RNA
CC   encapsidation sequences have been deleted from the non-coding regulatory
CC   sequences of HIV-1. The two or more sequences comprise a pol sequence
```

```
CC   having a mutation that inhibits one or more of the enzymatic activities
CC   of pol. The enzymatic activity is integrase activity, reverse
CC   transcriptase activity or protease activity. The enzymatic activity is
CC   inhibited by deleting a portion of the pol sequence or introducing one or
CC   more point mutations into the pol sequence. The present sequence is one
CC   such vector used to illustrate the invention.
XX
SQ   Sequence 10466 BP; 3316 A; 2205 C; 2539 G; 2405 T; 0 U; 1 Other;

  Query Match             31.6%;  Score 2027.6;  DB 9;  Length 10466;
  Best Local Similarity   87.4%;  Pred. No. 0;
  Matches 2407;  Conservative    1;  Mismatches   15;  Indels  331;  Gaps    4;

Qy       1654 ACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAA 1713
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Qy       1714 AATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGG 1773
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8101 AATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGG 8160

Qy       1774 ATCTTCTTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACC 1833
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Db       8161 ATCTTCTTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACC 8220

Qy       1834 GCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAC 1893
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Db       8221 GCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAC 8280

Qy       1894 TGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCA 1953
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Db       8281 TGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCA 8340

Qy       1954 CCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGT 2013
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Qy       2014 GGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACC 2073
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Db       8401 GGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACC 8460

Qy       2074 GGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCG 2133
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Db       8461 GGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCG 8520

Qy       2134 AACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC 2193
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Qy       2194 CGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCAC 2253
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Qy       2254 GAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCT 2313
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Qy       2314 CTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGC 2373
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Qy       2374 CAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTT 2433
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Qy       2434 TCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCATTAGTTATTAAT 2493

Db       8820 ------------------------------------------------------------ 8819

Qy       2494 AGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAAC 2553

Db       8820 ------------------------------------------------------------ 8819

Qy       2554 TTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAA 2613

Db       8820 ------------------------------------------------------------ 8819

Qy       2614 TGACGAGATCTGATATAGGTGACAGACGATATGAGGCTATATCGCCGATAGAGGCGACAT 2673

Db       8820 ------------------------------------------------------------ 8819

Qy       2674 CAAGCTGGCACATGGCCAATGCATATCGATCTATACATTGAATCAATATTGGCAATTAGC 2733

Db       8820 ------------------------------------------------------------ 8819

Qy       2734 CATATTAGTCATTGGTTATATAGCATAAATCAATATTGGCTATTGGCCATTGCATACGTT 2793
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Qy       2794 GTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAATATGACCGCCATGTTG 2853
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Qy       3332 TGGCACCAAAAATCAACGGGACTTTCCAAAAATGTCGTAATAACCCCGCCCCGTTGACGCAA 3391
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Qy       3632 TTTTTGGCTTGGGGCCTATACACCCCCGCTTCCTTATGCTATAGGTGATGGTATAGCTTA 3691
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RESULT 14
ADE06463
ID   ADE06463 standard; DNA; 10447 BP.
XX
AC   ADE06463;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Vector pGA1/IC2.
XX
KW   HIV infection; Anti-HIV; vaccine; ds.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   finger packaging sequences for viral RNA"
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XX
PF   10-MAR-2003; 2003WO-US007177.
XX
PR   08-MAR-2002; 2002US-00093953.
PR   03-JAN-2003; 2003US-00336566.
XX
PA   (UYEM-) UNIV EMORY.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Robinson HL,  Smith J,  Hua J,  Moss B;
XX
DR   WPI; 2003-731822/69.
XX
PT   A composition for generating an immune response against HIV comprises a
PT   vector comprising a vaccine insert encoding one or more antigens that
PT   elicit an immune response against HIV.
XX
PS   Example 12; Fig 14; 133pp; English.
XX
CC   The present invention relates to a composition comprising a first vector
CC   with a vaccine insert encoding one or more antigens that elicit an immune
CC   response against HIV or a first subtype or recombinant form; and a second
CC   vector comprising a vaccine insert encoding one or more antigens that
CC   elicit an immune response against an HIV of a second subtype or
CC   recombinant form. The composition is useful in generating an immune
CC   response against HIV. The insert of the first vector or the insert of the
CC   second vector comprises the sequences of two or more of: a gag, pol, env,
CC   tat, rev, nef, vif, vpr or vpu gene; or their mutants, and optionally;
CC   non-coding regulatory sequences of the HIV genome. At least one of the
CC   two or more sequences comprises mutations that limit the encapsidation of
CC   viral RNA, or a gag sequence having a mutation in one or more of the
CC   sequences encoding a zinc finger. All or part of cis-acting RNA
CC   encapsidation sequences have been deleted from the non-coding regulatory
CC   sequences of HIV-1. The two or more sequences comprise a pol sequence
CC   having a mutation that inhibits one or more of the enzymatic activities
CC   of pol. The enzymatic activity is integrase activity, reverse
CC   transcriptase activity or protease activity. The enzymatic activity is
CC   inhibited by deleting a portion of the pol sequence or introducing one or
CC   more point mutations into the pol sequence. The present sequence is one
CC   such vector used to illustrate the invention.
XX
SQ   Sequence 10447 BP; 3304 A; 2213 C; 2548 G; 2381 T; 0 U; 1 Other;

  Query Match             31.6%;  Score 2027.2;  DB 9;  Length 10447;
  Best Local Similarity   87.4%;  Pred. No. 0;
  Matches 2406;  Conservative    1;  Mismatches   14;  Indels  331;  Gaps    4;

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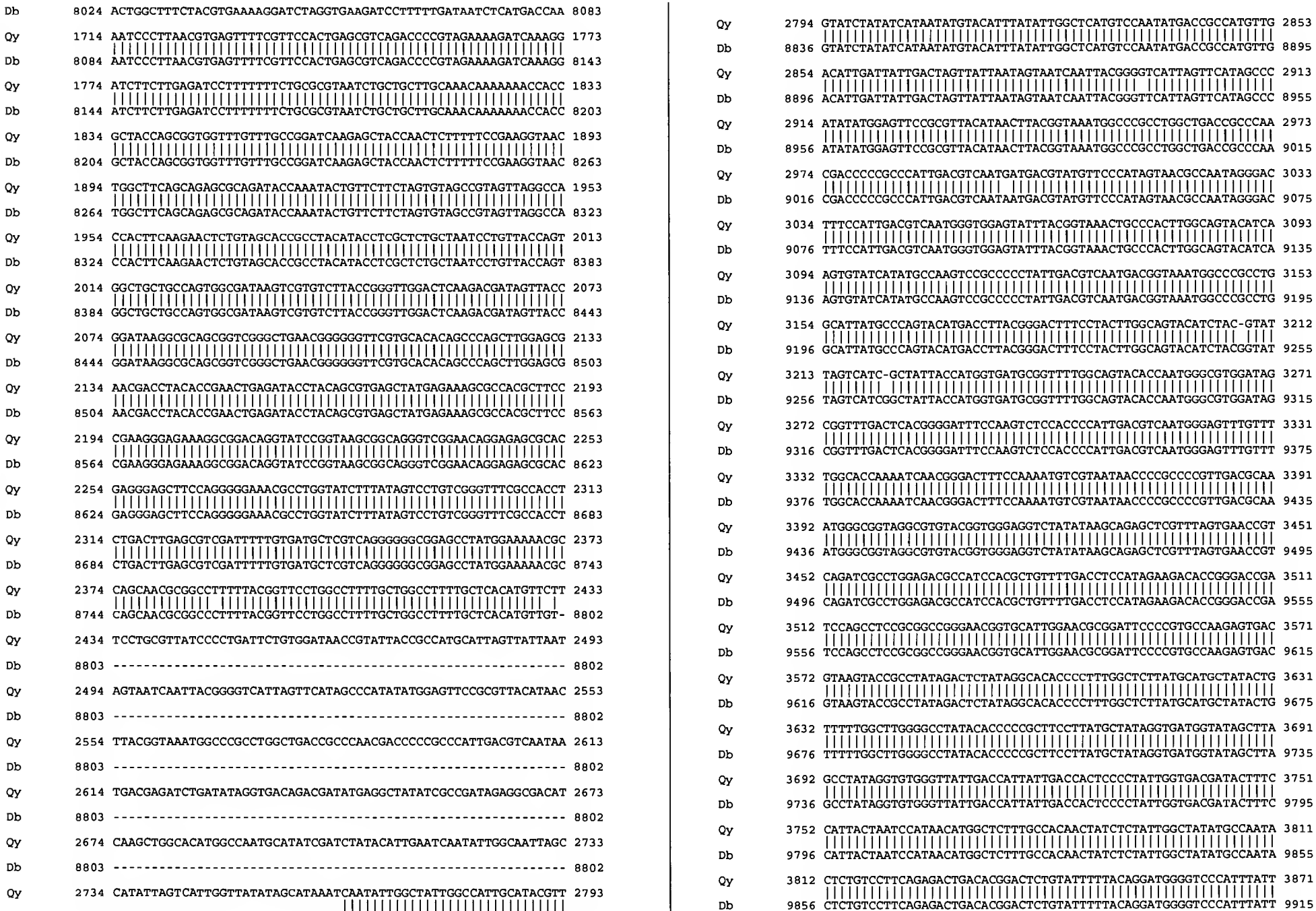
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RESULT 15

ADE06462

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ID   ADE06462 standard; DNA; 10447 BP.
XX
AC   ADE06462;
XX
DT   29-JAN-2004  (first entry)
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DE   Vector pGA1/IC25.
XX
KW   HIV infection; Anti-HIV; vaccine; ds.
XX
OS   Synthetic.
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PN   WO2003076591-A2.
XX
PD   18-SEP-2003.
XX
PF   10-MAR-2003; 2003WO-US007177.
XX
PR   08-MAR-2002; 2002US-00093953.
PR   03-JAN-2003; 2003US-00336566.
XX
PA   (UYEM-) UNIV EMORY.
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Robinson HL,  Smith J,  Hua J,  Moss B;
XX
DR   WPI; 2003-731822/69.
XX
PT   A composition for generating an immune response against HIV comprises a
PT   vector comprising a vaccine insert encoding one or more antigens that
PT   elicit an immune response against HIV.
XX
PS   Example 11; Fig 13; 133pp; English.
XX
CC   The present invention relates to a composition comprising a first vector
CC   with a vaccine insert encoding one or more antigens that elicit an immune
CC   response against HIV or a first subtype or recombinant form; and a second
CC   vector comprising a vaccine insert encoding one or more antigens that
CC   elicit an immune response against an HIV of a second subtype or
CC   recombinant form. The composition is useful in generating an immune
CC   response against HIV. The insert of the first vector or the insert of the
CC   second vector comprises the sequences of two or more of: a gag, pol, env,
CC   tat, rev, nef, vif, vpr or vpu gene; or their mutants, and optionally;
CC   non-coding regulatory sequences of the HIV genome. At least one of the
CC   two or more sequences comprises mutations that limit the encapsidation of
CC   viral RNA, or a gag sequence having a mutation in one or more of the
CC   sequences encoding a zinc finger. All or part of cis-acting RNA
CC   encapsidation sequences have been deleted from the non-coding regulatory
CC   sequences of HIV-1. The two or more sequences comprise a pol sequence
CC   having a mutation that inhibits one or more of the enzymatic activities
CC   of pol. The enzymatic activity is integrase activity, reverse
CC   transcriptase activity or protease activity. The enzymatic activity is
CC   inhibited by deleting a portion of the pol sequence or introducing one or
CC   more point mutations into the pol sequence. The present sequence is one
CC   such vector used to illustrate the invention.
XX
SQ   Sequence 10447 BP; 3305 A; 2213 C; 2547 G; 2381 T; 0 U; 1 Other;
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Query Match 31.6%; Score 2027.2; DB 9; Length 10447;
Best Local Similarity 87.4%; Pred. No. 0;
Matches 2406; Conservative 1; Mismatches 14; Indels 331; Gaps 4;

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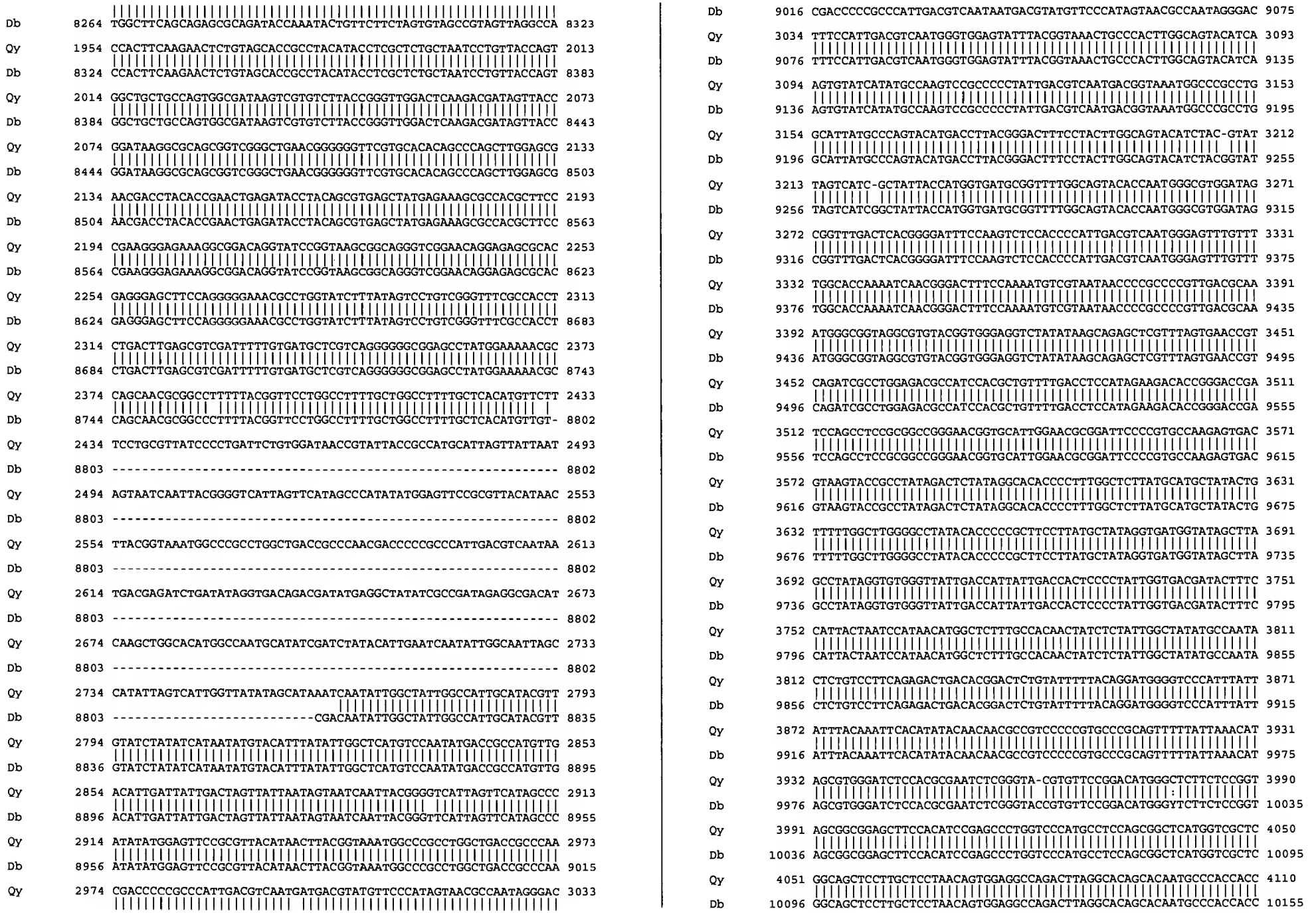

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Job time : 2213 secs

GenCore version 5.1.6

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	6	2378.8	37.1	5488	6	AX776821	AX776821 Sequence
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO03031630.
ACCESSION AX743953
VERSION AX743953.1 GI:30722650
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Orsini,G.
TITLE Multi-cistronic vectors for gene transfer protocols
JOURNAL Patent: WO 03031630-A 1 17-APR-2003;
Keryos Spa (IT)

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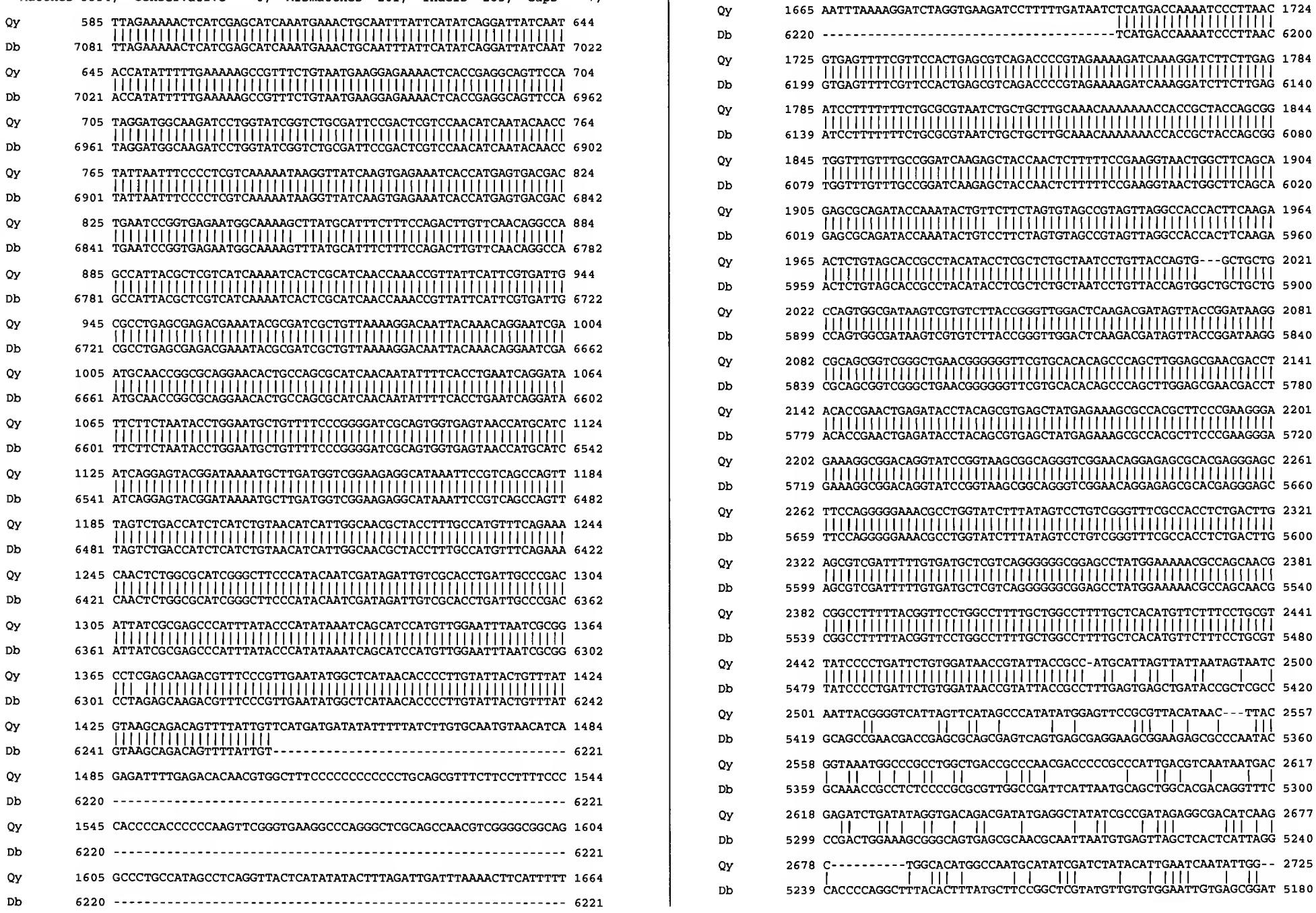
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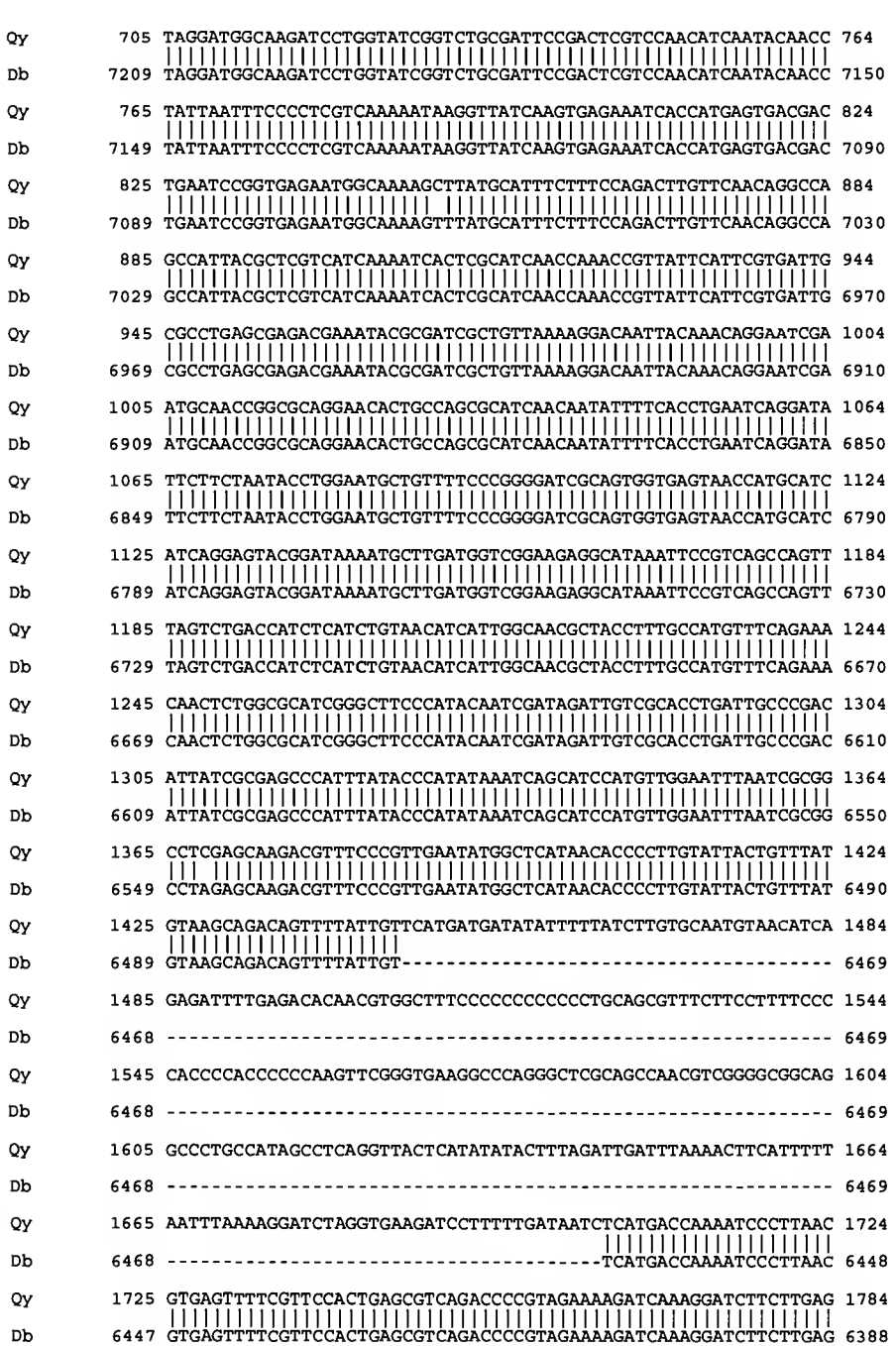
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VERSION     AX776820.1  GI:32694262
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  AUTHORS   Haynes,J.R. and Arrington,J.E.
  TITLE     Nucleic acid adjuvants
  JOURNAL   Patent: WO 03004055-A 2 16-JAN-2003;
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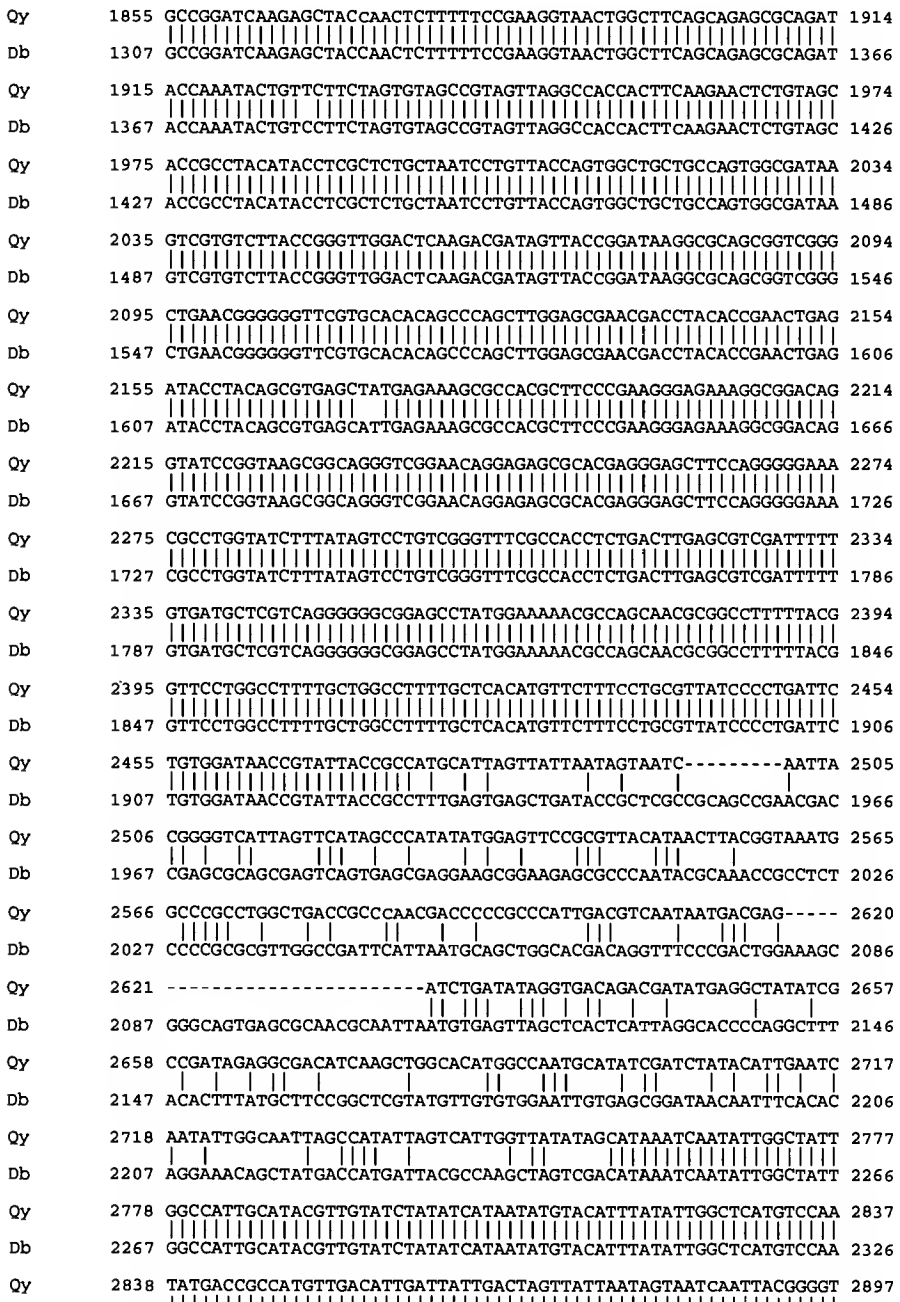

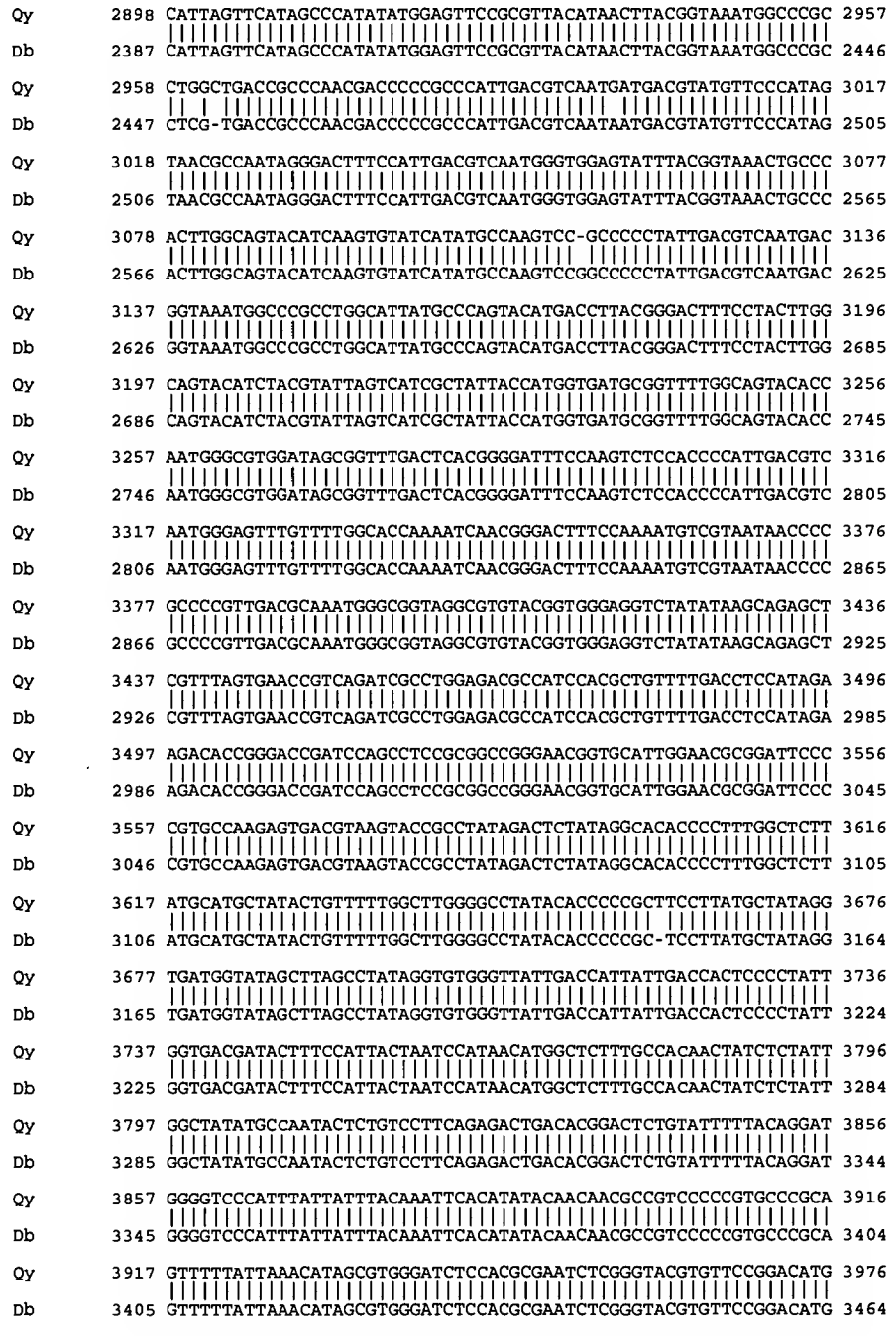

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DEFINITION  Sequence 5 from Patent WO03004055.
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VERSION     AX776823.1  GI:32694265
KEYWORDS    .
SOURCE      unidentified
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            unclassified.
REFERENCE   1
  AUTHORS   Haynes,J.R. and Arrington,J.E.
  TITLE     Nucleic acid adjuvants
  JOURNAL   Patent: WO 03004055-A 5 16-JAN-2003;
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ORIGIN

  Query Match             37.1%;  Score 2378.8;  DB 6;  Length 5089;
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  Matches 2598;  Conservative    0;  Mismatches  197;  Indels   41;  Gaps    6;

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VERSION     AX776821.1  GI:32694263
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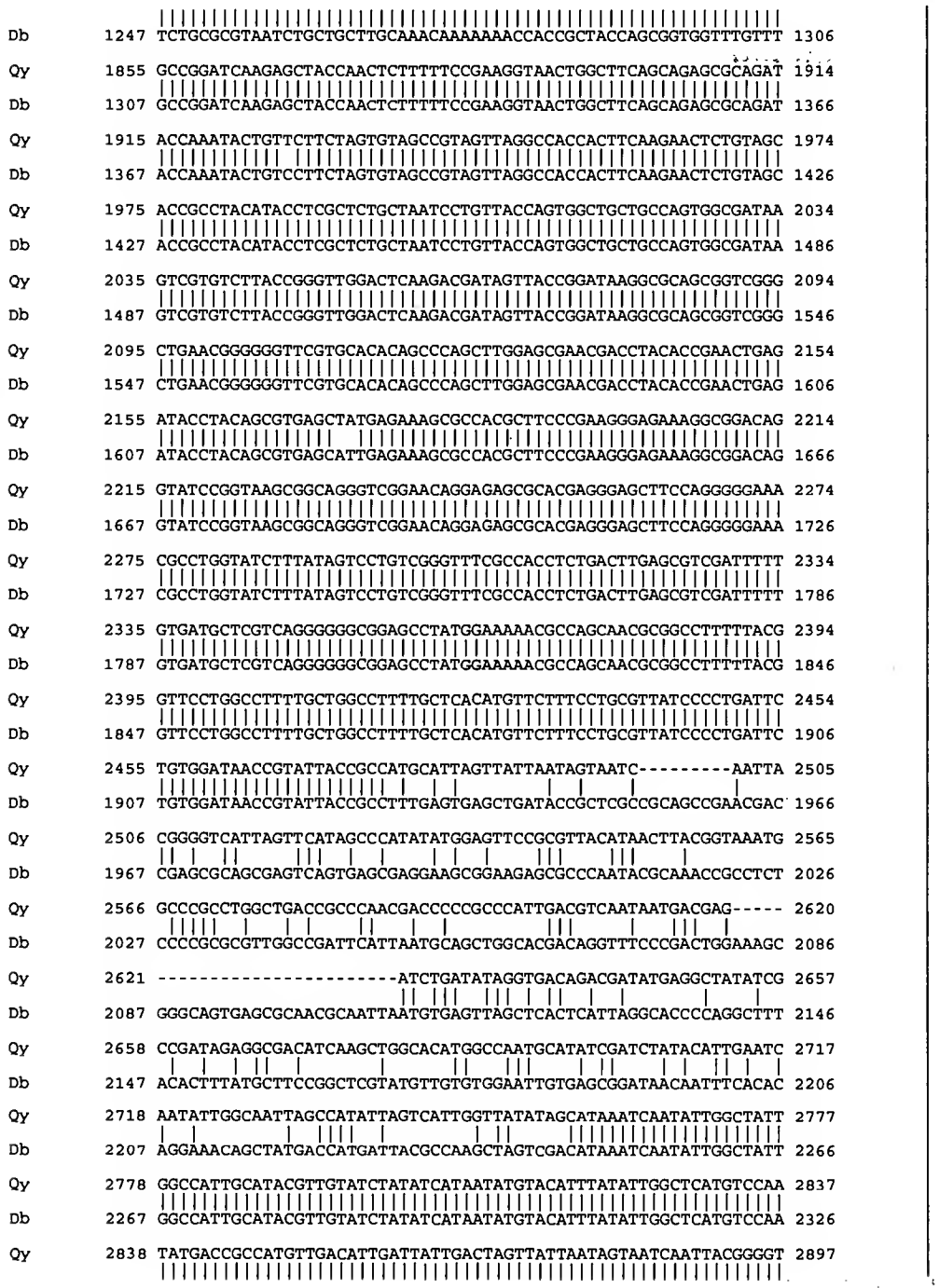
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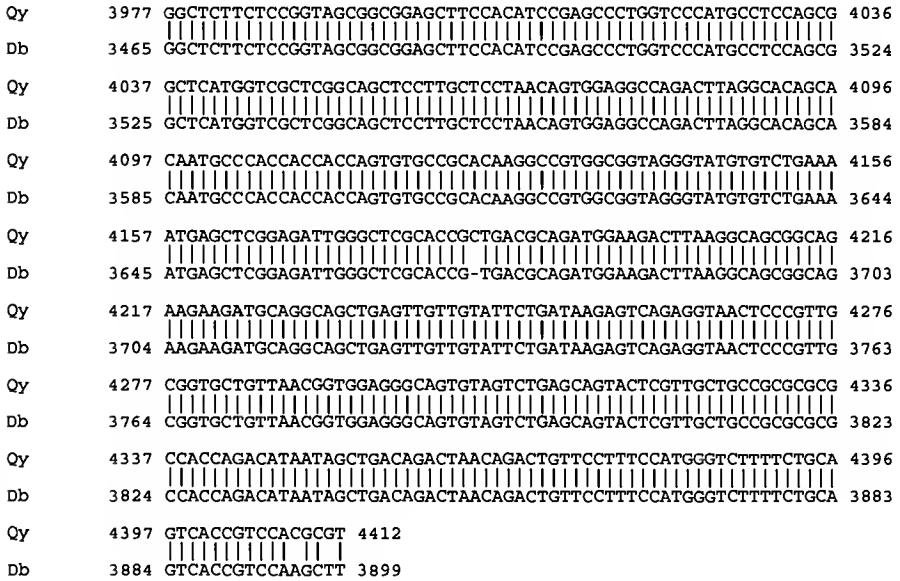

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VERSION AX776824.1 GI:32694266
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SOURCE unidentified
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AUTHORS Haynes,J.R. and Arrington,J.E.
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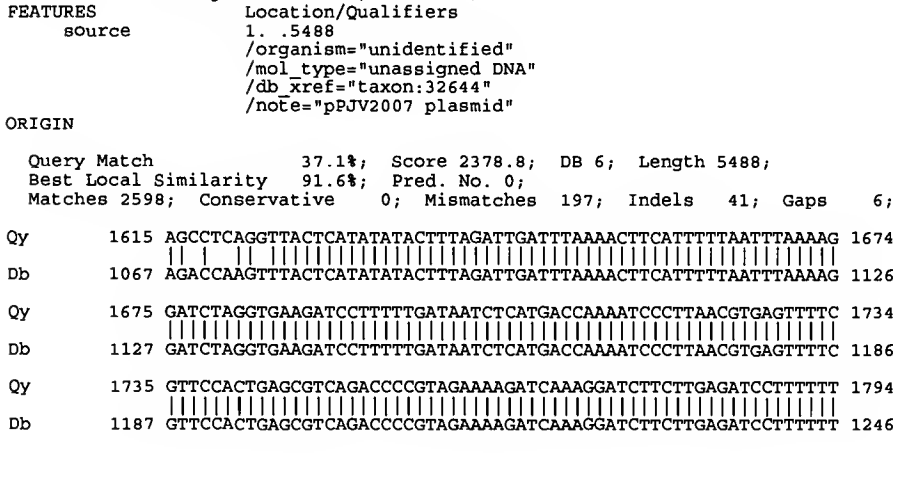

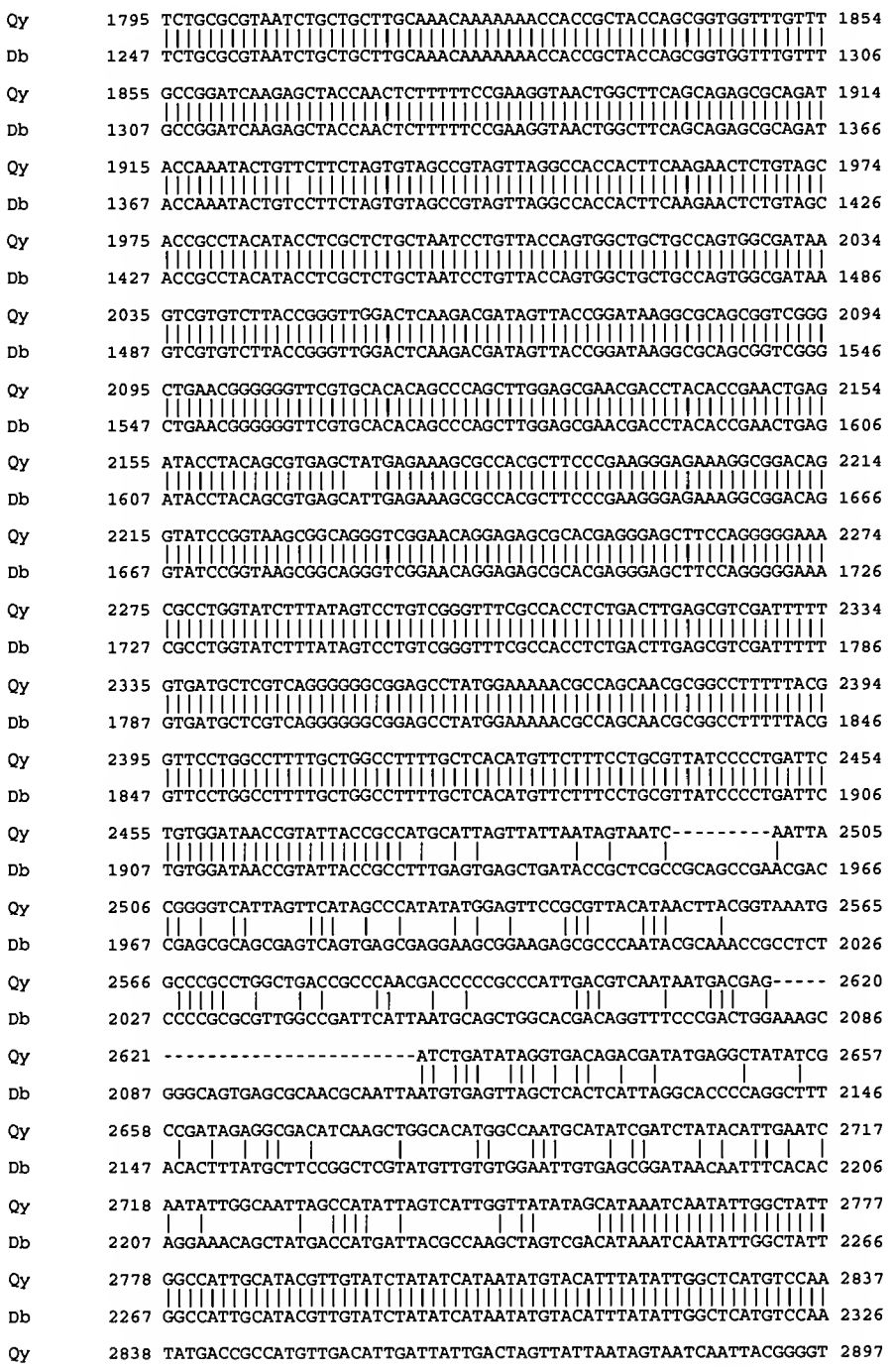

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Db       3405 GTTTTTATTAAACATAGCGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATG 3464

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Qy       4037 GCTCATGGTCGCTCGGCAGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCA 4096
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Qy       4277 CGGTGCTGTTAACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCG 4336
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LOCUS       AX776819               5500 bp    DNA     linear   PAT 14-JUL-2003
DEFINITION  Sequence 1 from Patent WO03004055.
ACCESSION   AX776819
VERSION     AX776819.1  GI:32694261
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Haynes,J.R. and Arrington,J.E.
  TITLE     Nucleic acid adjuvants
  JOURNAL   Patent: WO 03004055-A 1 16-JAN-2003;
            Powderject Vaccines, Inc. (US)
FEATURES             Location/Qualifiers
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  Query Match             37.1%;  Score 2378.8;  DB 6;  Length 5500;
  Best Local Similarity   91.6%;  Pred. No. 0;
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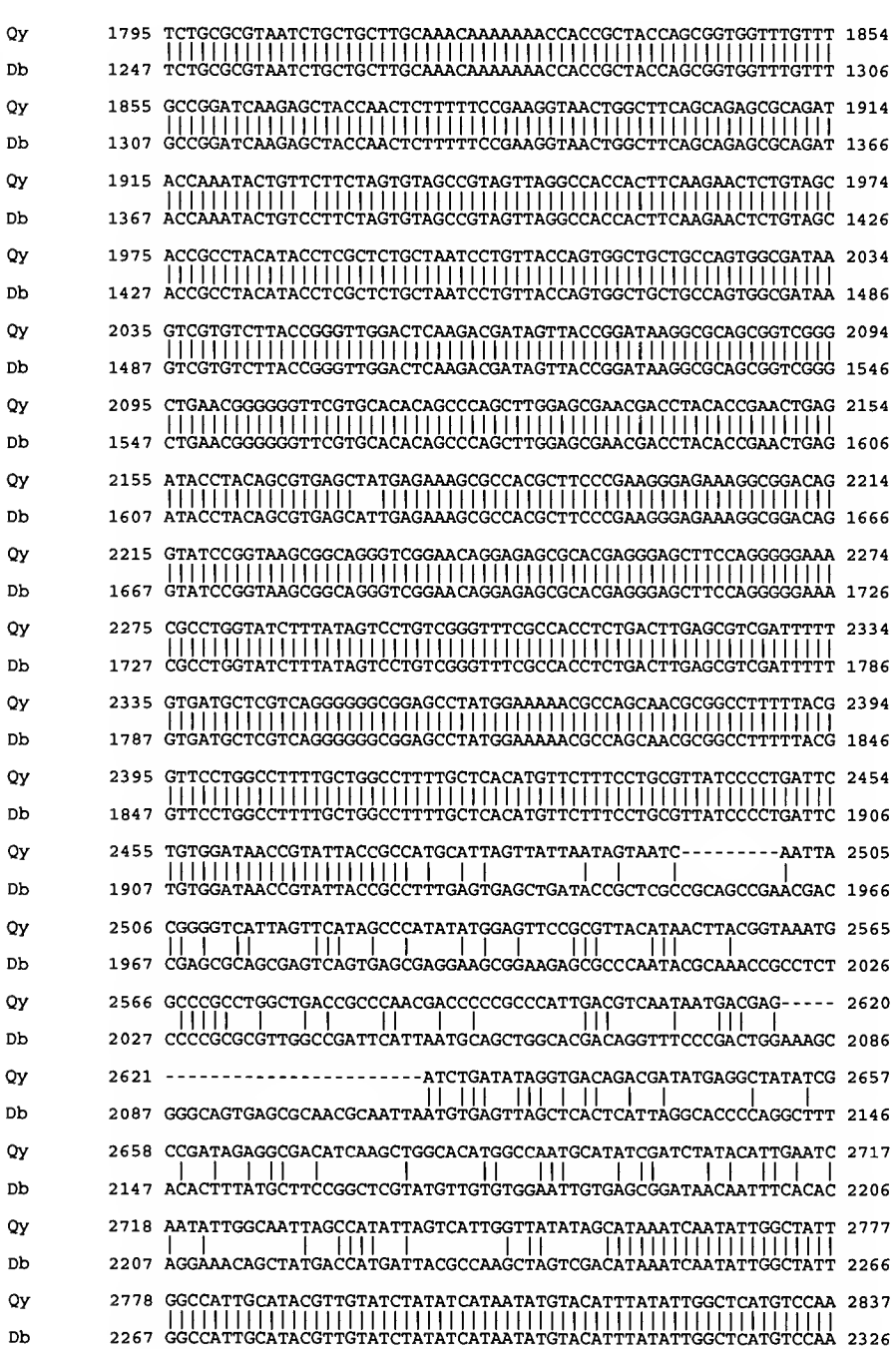
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Qy 2658 CCGATAGAGGCGACATCAAGCTGGCACATGGCCAATGCATATCGATCTATACATTGAATC 2717
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Qy 2718 AATATTGGCAATTAGCCATATTAGTCATTGGTTATATAGCATAAATCAATATTGGCTATT 2777
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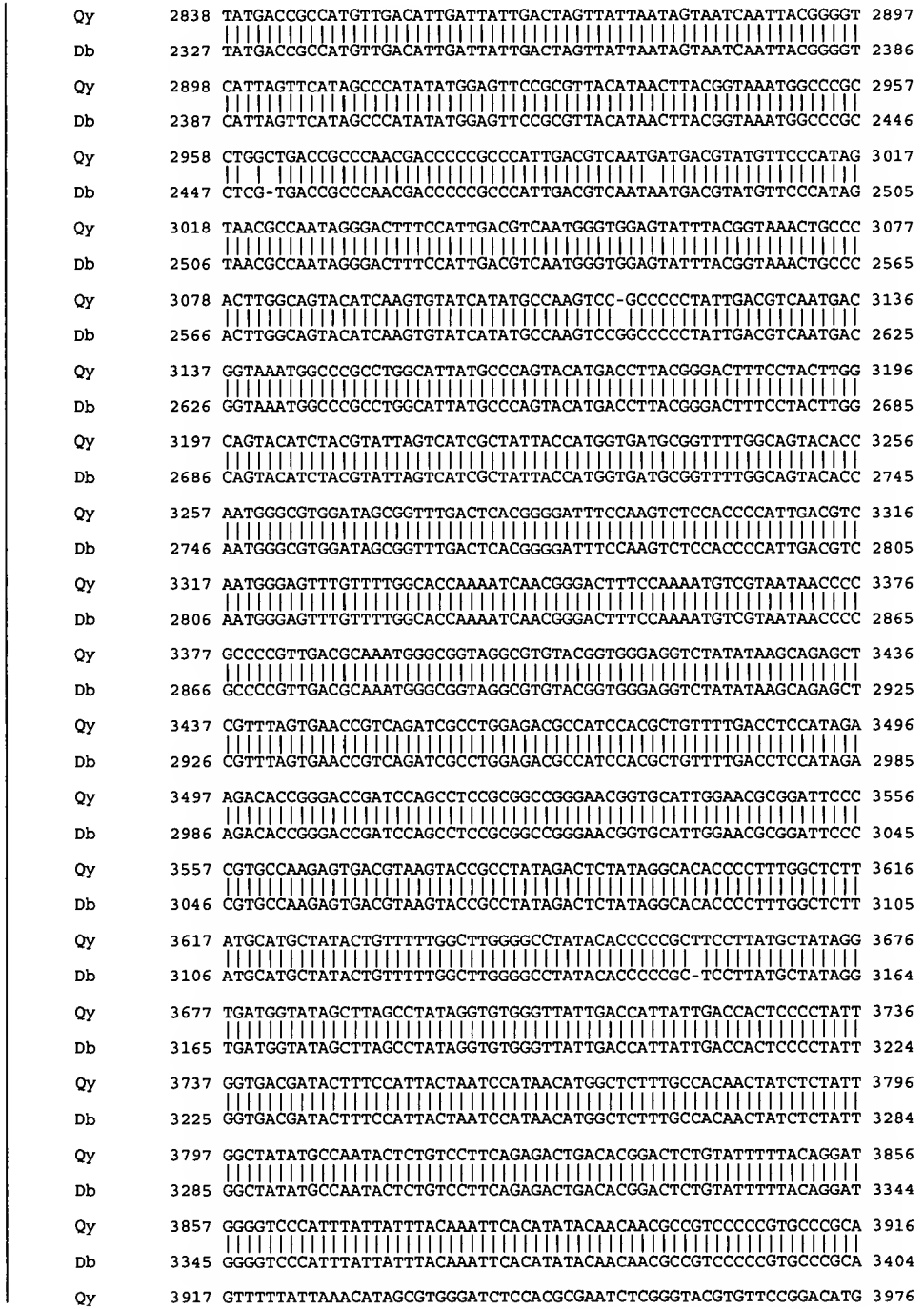
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Qy       4337 CCACCAGACATAATAGCTGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCA 4396
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Qy       4397 GTCACCGTCCACGCGT 4412
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RESULT 9
AX776822
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DEFINITION  Sequence 4 from Patent WO03004055.
ACCESSION   AX776822
VERSION     AX776822.1  GI:32694264
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Haynes,J.R. and Arrington,J.E.
  TITLE     Nucleic acid adjuvants
  JOURNAL   Patent: WO 03004055-A 4 16-JAN-2003;
            Powderject Vaccines, Inc. (US)
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Qy       2778 GGCCATTGCATACGTTGTATCTATATCATAATATGTACATTTATATTGGCTCATGTCCAA 2837
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VERSION     AF430344.1  GI:16798502
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SOURCE      synthetic construct
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  TITLE     Multiprotein-expressing DNA Component for a DNA/MVA Vaccine for
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  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 9918)
  AUTHORS   Smith,J.M. and Robinson,H.L.
  TITLE     Direct Submission
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ORIGIN
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Best Local Similarity 87.5%;  Pred. No. 0;
Matches 2409;  Conservative    0;  Mismatches   17;  Indels  328;  Gaps    5;

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Db      8278 ---------------------------------------------------------- 8277

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Qy       3574 AAGTACCGCCTATAGACTCTATAGGCACACCCCTTTGGCTCTTATGCATGCTATACTGTT 3633
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Db       9266 TTACTAATCCATAACATGGCTCTTTGCCACAACTATCTCTATTGGCTATATGCCAATACT 9325

Qy       3814 CTGTCCTTCAGAGACTGACACGGACTCTGTATTTTTACAGGATGGGGTCCCATTTATTAT 3873
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Qy       3934 CGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGGGCTCTTCTCCGGTAGC 3993
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Db       9446 CGTGGGATCTCCACGCGAATCTCGGGTACGTGTTCCGGACATGGGCTCTTCTCCGGTAGC 9505

Qy       3994 GGCGGAGCTTCCACATCCGAGCCCTGGTCCCATGCCTCCAGCGGCTCATGGTCGCTCGGC 4053
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Qy       4054 AGCTCCTTGCTCCTAACAGTGGAGGCCAGACTTAGGCACAGCACAATGCCCACCACCACC 4113
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Qy       4234 TGAGTTGTTGTATTCTGATAAGAGTCAGAGGTAACTCCCGTTGCGGTGCTGTTAACGGTG 4293
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Qy       4294 GAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGCGCCACCAGACATAATAGC 4353
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Qy       4354 TGACAGACTAACAGACTGTTCCTTTCCATGGGTCTTTTCTGCAGTCACCGTCCA 4407
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RESULT 11
AX138932
LOCUS       AX138932               5108 bp    DNA     linear   PAT 31-MAY-2001
DEFINITION  Sequence 51 from Patent EP1052286.
ACCESSION   AX138932
VERSION     AX138932.1  GI:14274637
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Morsey,M.A. and Sheppard,M.G.
  TITLE     Growth hormone and growth hormone releasing hormone compositions
  JOURNAL   Patent: EP 1052286-A 51 15-NOV-2000;
            Pfizer Products Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             31.3%;  Score 2008.6;  DB 6;  Length 5108;
  Best Local Similarity   74.2%;  Pred. No. 0;
  Matches 3058;  Conservative    0;  Mismatches  239;  Indels  826;  Gaps    8;

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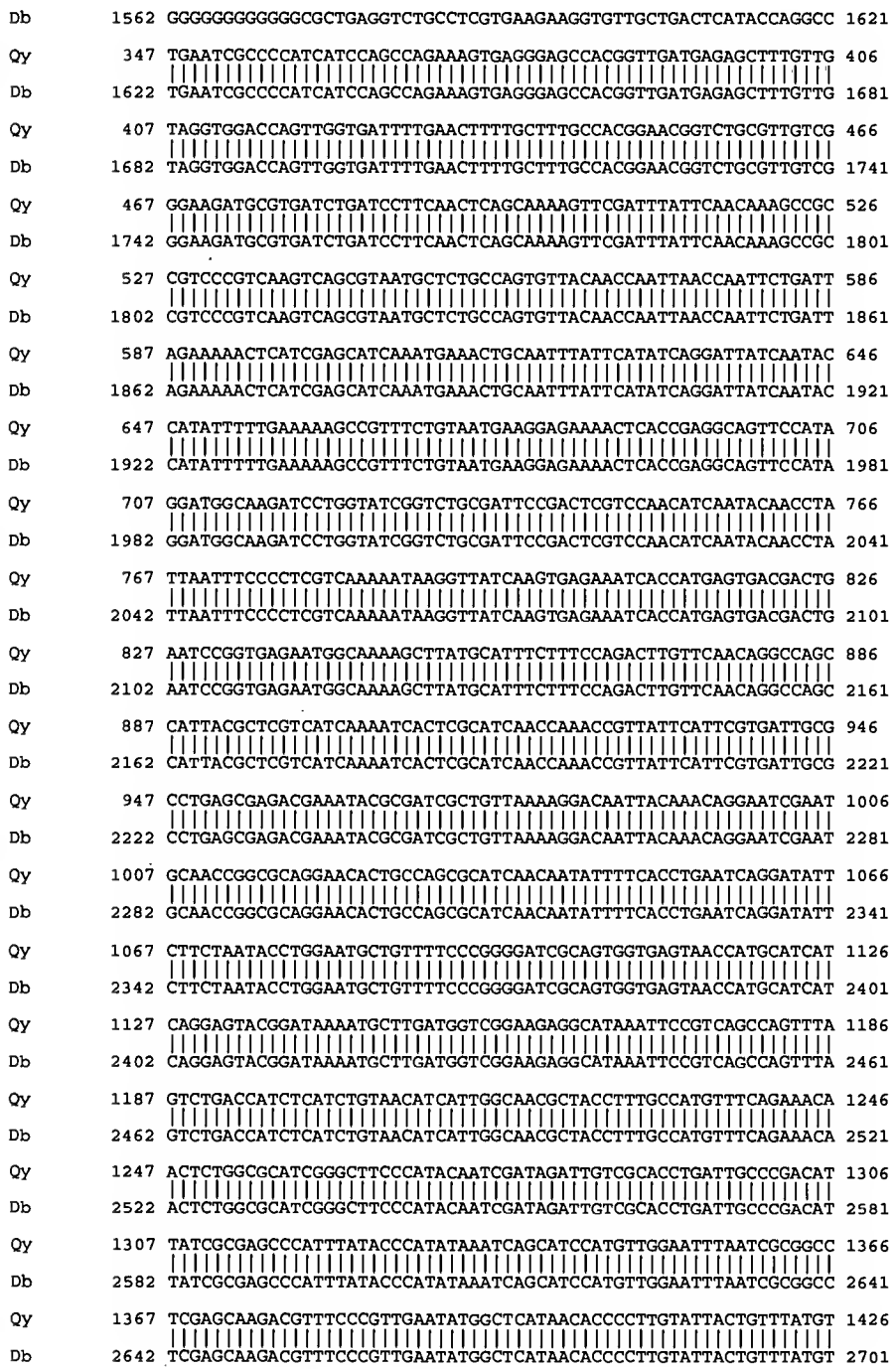
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Qy 1367 TCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTATGT 1426
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Qy 1967 TCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGT 2026
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Qy 2027 GGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAG 2086
Db 2970 GCCCTTTCGTCCT---------- 2982
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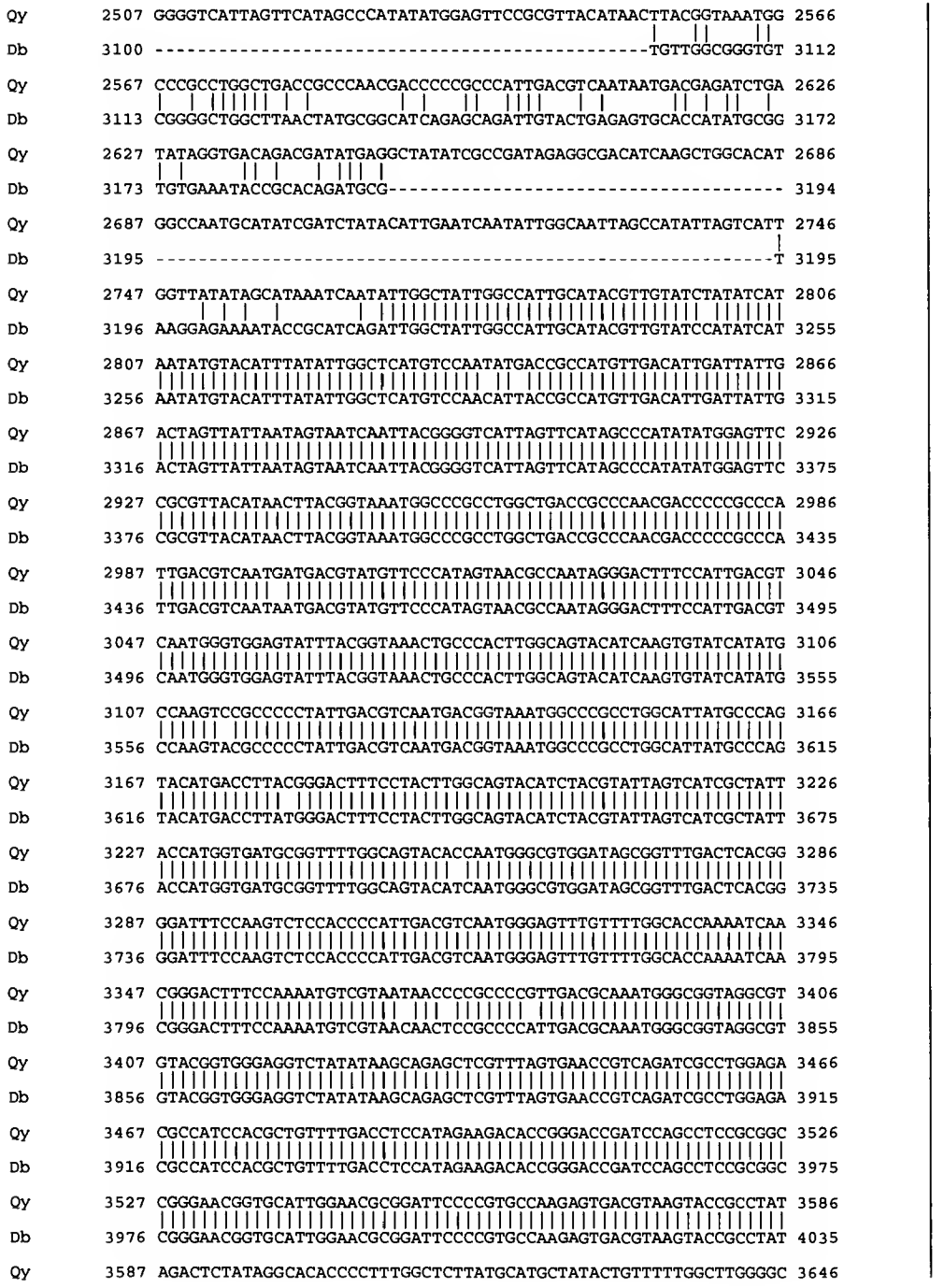

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RESULT 12
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LOCUS       AX138933               5108 bp    DNA     linear   PAT 30-MAY-2001
DEFINITION  Sequence 52 from Patent EP1052286.
ACCESSION   AX138933
VERSION     AX138933.1  GI:14274638
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Morsey,M.A. and Sheppard,M.G.
  TITLE     Growth hormone and growth hormone releasing hormone compositions
  JOURNAL   Patent: EP 1052286-A 52 15-NOV-2000;
            Pfizer Products Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .5108
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  Query Match           31.3%;  Score 2008.6;  DB 6;  Length 5108;
  Best Local Similarity  74.2%;  Pred. No. 0;
  Matches 3058;  Conservative    0;  Mismatches  239;  Indels  826;  Gaps    8;

Qy        287 GGGGGGGGGGGGGCGCTGAGGTCTGCCTCGTGAAGAAGGTGTTGCTGACTCATACCAGGCC 346
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Qy        347 TGAATCGCCCCATCATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGAGCTTTGTTG 406
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Qy        407 TAGGTGGACCAGTTGGTGATTTTGAACTTTTGCTTTGCCACGGAACGGTCTGCGTTGTCG 466
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Qy        467 GGAAGATGCGTGATCTGATCCTTCAACTCAGCAAAAGTTCGATTTATTCAACAAAGCCGC 526
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Qy        527 CGTCCCGTCAAGTCAGCGTAATGCTCTGCCAGTGTTACAACCAATTAACCAATTCTGATT 586
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Qy       1007 GCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATT 1066
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Qy       2087 CGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACC 2146
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Qy       2147 GAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAG 2206
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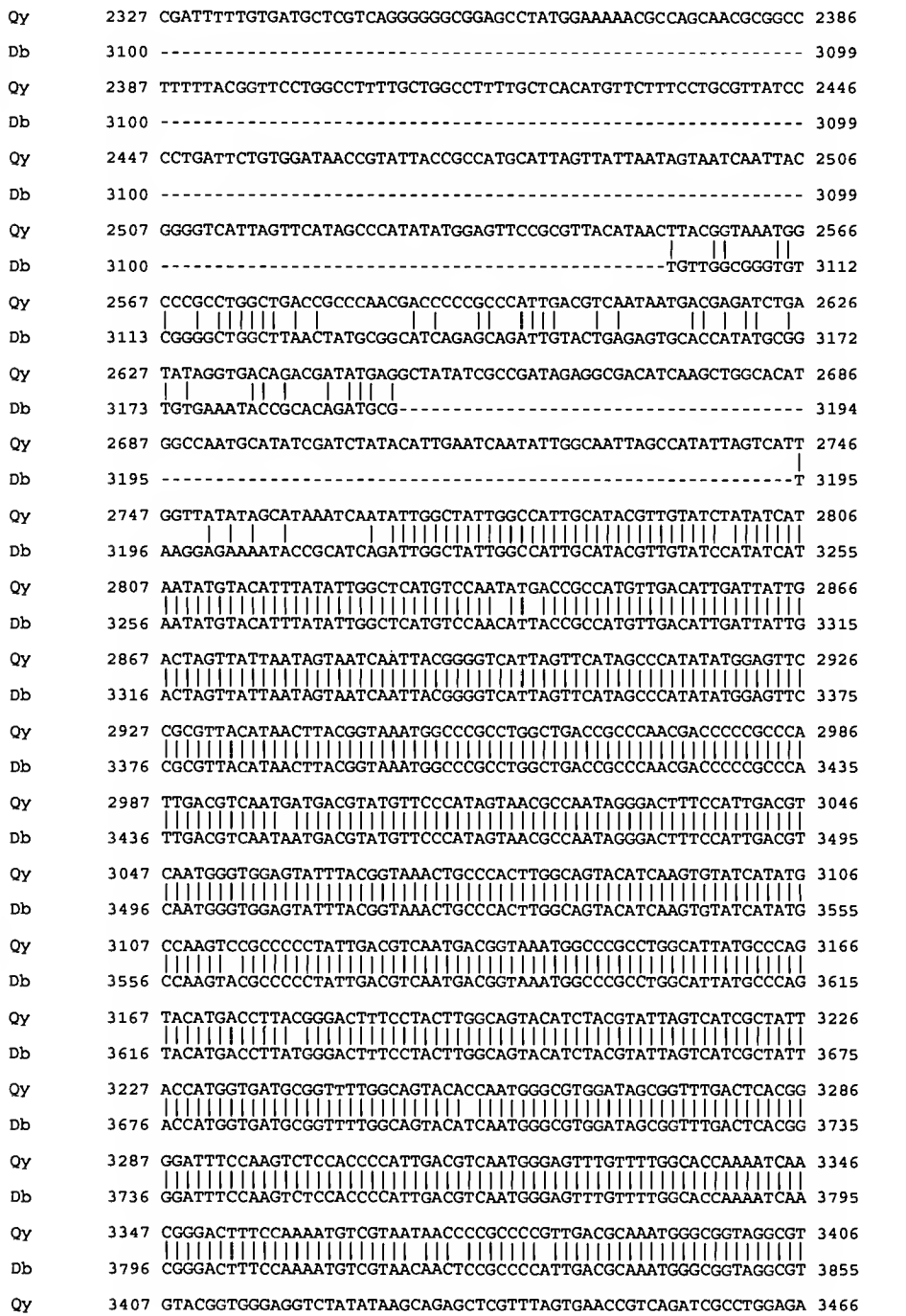

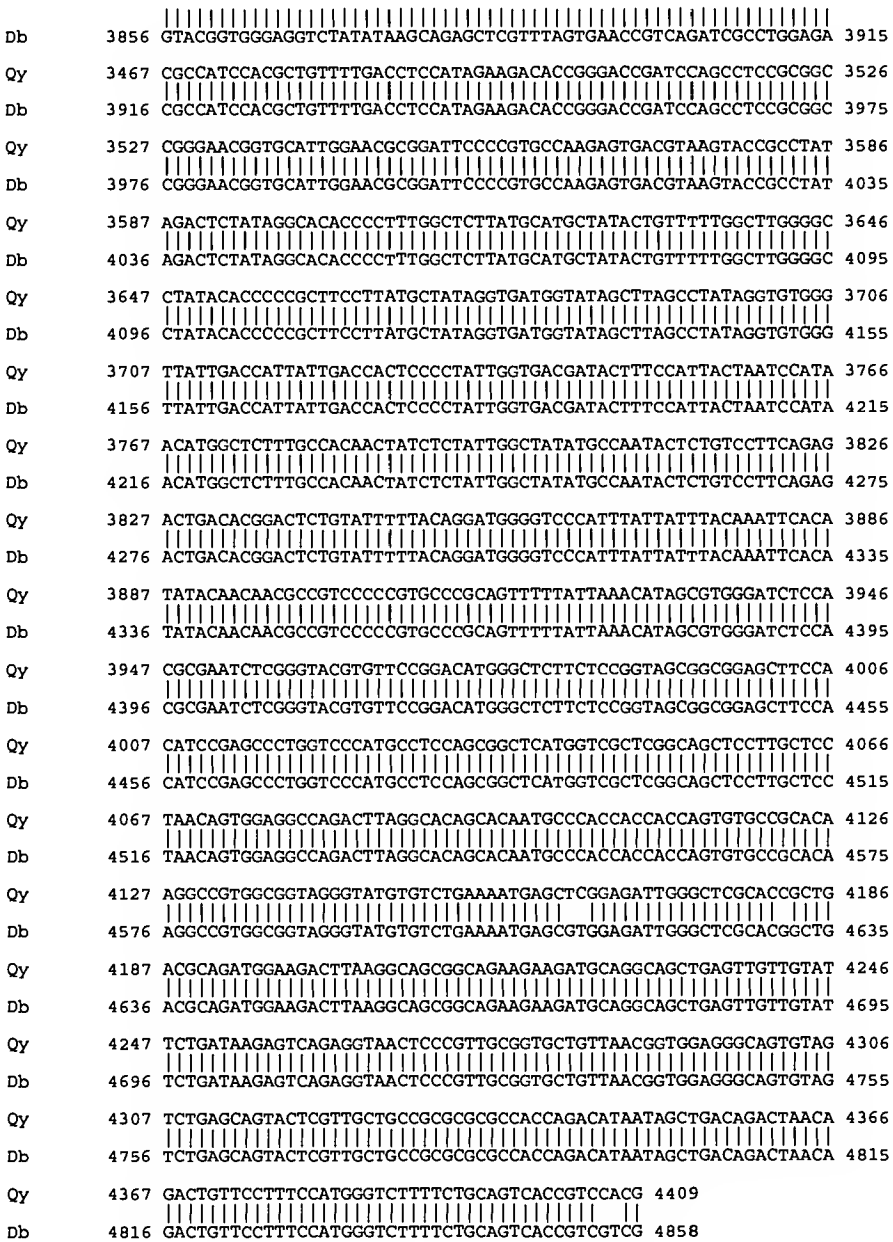

RESULT 13
BD000697
LOCUS BD000697 5108 bp DNA linear PAT 31-JAN-2002
DEFINITION Growth hormone and growth hormone-releasing hormone composition.
ACCESSION BD000697

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VERSION     BD000697.1  GI:18623810
KEYWORDS    JP 2000350590-A/50.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 5108)
  AUTHORS   Morsey,M.A. and George,M.
  TITLE     Growth hormone and growth hormone-releasing hormone composition
  JOURNAL   Patent: JP 2000350590-A 50 19-DEC-2000;
            PFIZER PROD INC
COMMENT     OS   Artificial Sequence
            PN   JP 2000350590-A/50
            PD   19-DEC-2000
            PF   12-APR-2000 JP 2000111120
            PR   12-APR-1999 US    60/128830
            PI   MOHAMMED ALI MORSEY,MICHAEL GEORGE
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ORIGIN

  Query Match           31.3%;  Score 2008.6;  DB 6;  Length 5108;
  Best Local Similarity   74.2%;  Pred. No. 0;
  Matches 3058;  Conservative    0;  Mismatches  239;  Indels  826;  Gaps    8;

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Qy        347 TGAATCGCCCCATCATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGAGCTTTGTTG 406
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Db       1622 TGAATCGCCCCATCATCCAGCCAGAAAGTGAGGGAGCCACGGTTGATGAGAGCTTTGTTG 1681

Qy        407 TAGGTGGACCAGTTGGTGATTTTGAACTTTTGCTTTGCCACGGAACGGTCTGCGTTGTCG 466
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Db       1682 TAGGTGGACCAGTTGGTGATTTTGAACTTTTGCTTTGCCACGGAACGGTCTGCGTTGTCG 1741

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Qy        527 CGTCCCGTCAAGTCAGCGTAATGCTCTGCCAGTGTTACAACCAATTAACCAATTCTGATT 586
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Qy        587 AGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATAC 646
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Qy        647 CATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATA 706
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Qy        707 GGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTA 766
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Qy        887 CATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCG 946
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Qy        947 CCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAAT 1006
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Db       2342 CTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCAT 2401

Qy       1127 CAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTA 1186
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Db       2402 CAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTA 2461

Qy       1187 GTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACA 1246
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Qy       1247 ACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACAT 1306
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Qy       1307 TATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCC 1366
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Qy       1367 TCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTATGT 1426
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Db       2642 TCGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTGTATTACTGTTTATGT 2701

Qy       1427 AAGCAGACAGTTTTATTGTTCATGATGATATATTTTTATCTTGTGCAATGTAACATCAGA 1486
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Qy       1547 CCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGC 1606
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Db       2798 ---------------------------------------------------------- 2797

Qy       1607 CCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAA 1666
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Db       2798 ----------------------------ATTATTGAAGCATTTATCAGGGTTATTGTCT 2828

Qy       1667 TTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGT 1726
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Qy       1727 GAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGAT 1786
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Qy       1787 CCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTG 1846
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Qy       1847 GTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGA 1906
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Db       2936 ---------------------------------------------------------- 2935

Qy       1907 GCGCAGATACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAC 1966
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Db       2342 CTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCAT 2401

Qy       1127 CAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTA 1186
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Qy       1247 ACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACAT 1306
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Qy       1307 TATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCC 1366
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Qy       1787 CCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTG 1846
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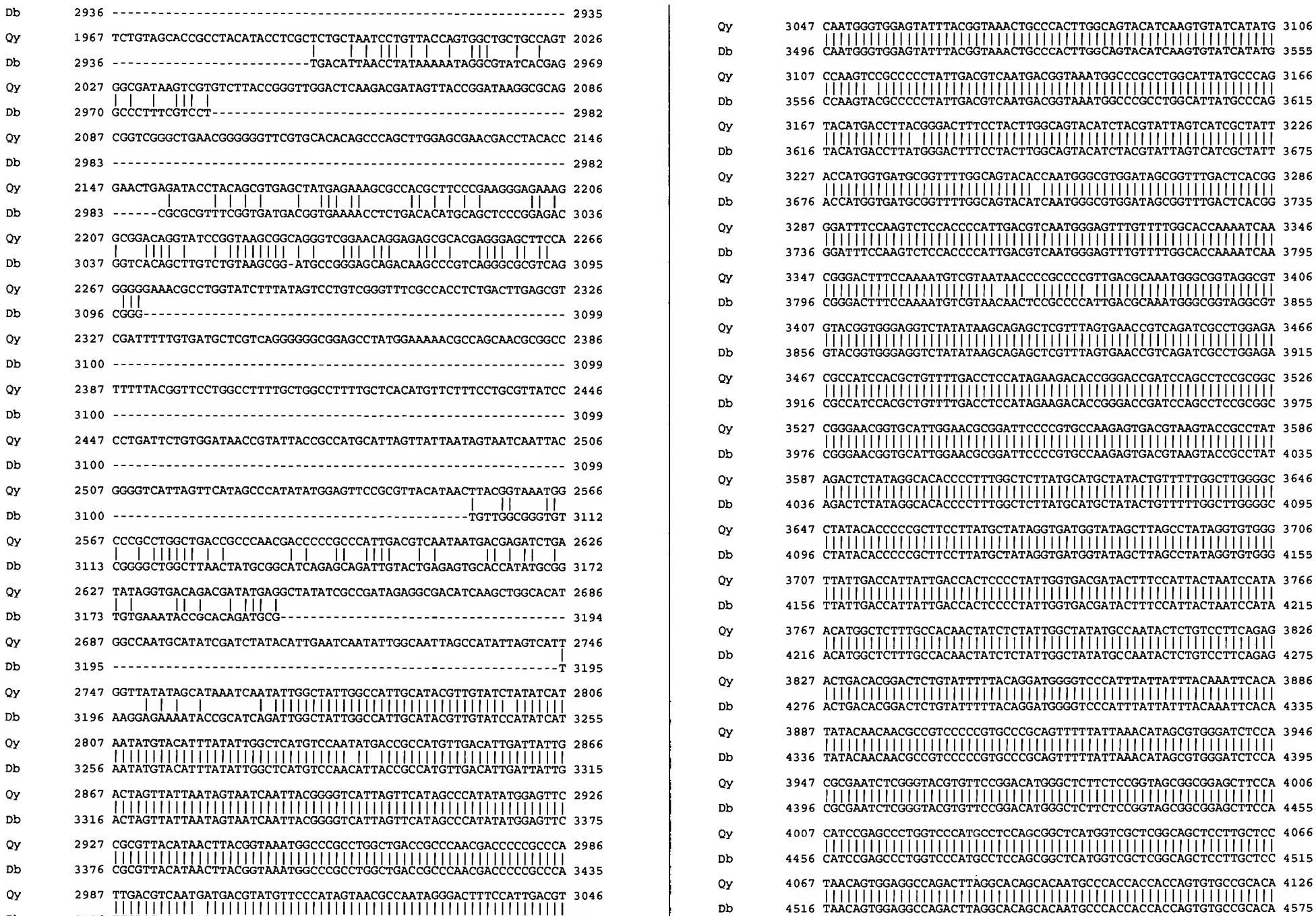

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RESULT 14
BD000698
LOCUS       BD000698                5108 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Growth hormone and growth hormone-releasing hormone composition.
ACCESSION   BD000698
VERSION     BD000698.1  GI:18623811
KEYWORDS    JP 2000350590-A/51.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 5108)
  AUTHORS   Morsey,M.A. and George,M.
  TITLE     Growth hormone and growth hormone-releasing hormone composition
  JOURNAL   Patent: JP 2000350590-A 51 19-DEC-2000;
            PFIZER PROD INC
COMMENT     OS   Artificial Sequence
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            PD   19-DEC-2000
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            PI   MOHAMMED ALI MORSEY,MICHAEL GEORGE
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            PC   A61K37/43,C12N5/00,(C12N5/00,C12R1:91)
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           31.3%;  Score 2008.6;  DB 6;  Length 5108;
  Best Local Similarity   74.2%;  Pred. No. 0;
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Qy        467 GGAAGATGCGTGATCTGATCCTTCAACTCAGCAAAAGTTCGATTTATTCAACAAAGCCGC 526
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Db       1922 CATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATA 1981

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Qy        827 AATCCGGTGAGAATGGCAAAAGCTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGC 886
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Qy        887 CATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCG 946
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Qy       1067 CTTCTAATACCTGGAATGCTGTTTTCCCGGGGATCGCAGTGGTGAGTAACCATGCATCAT 1126
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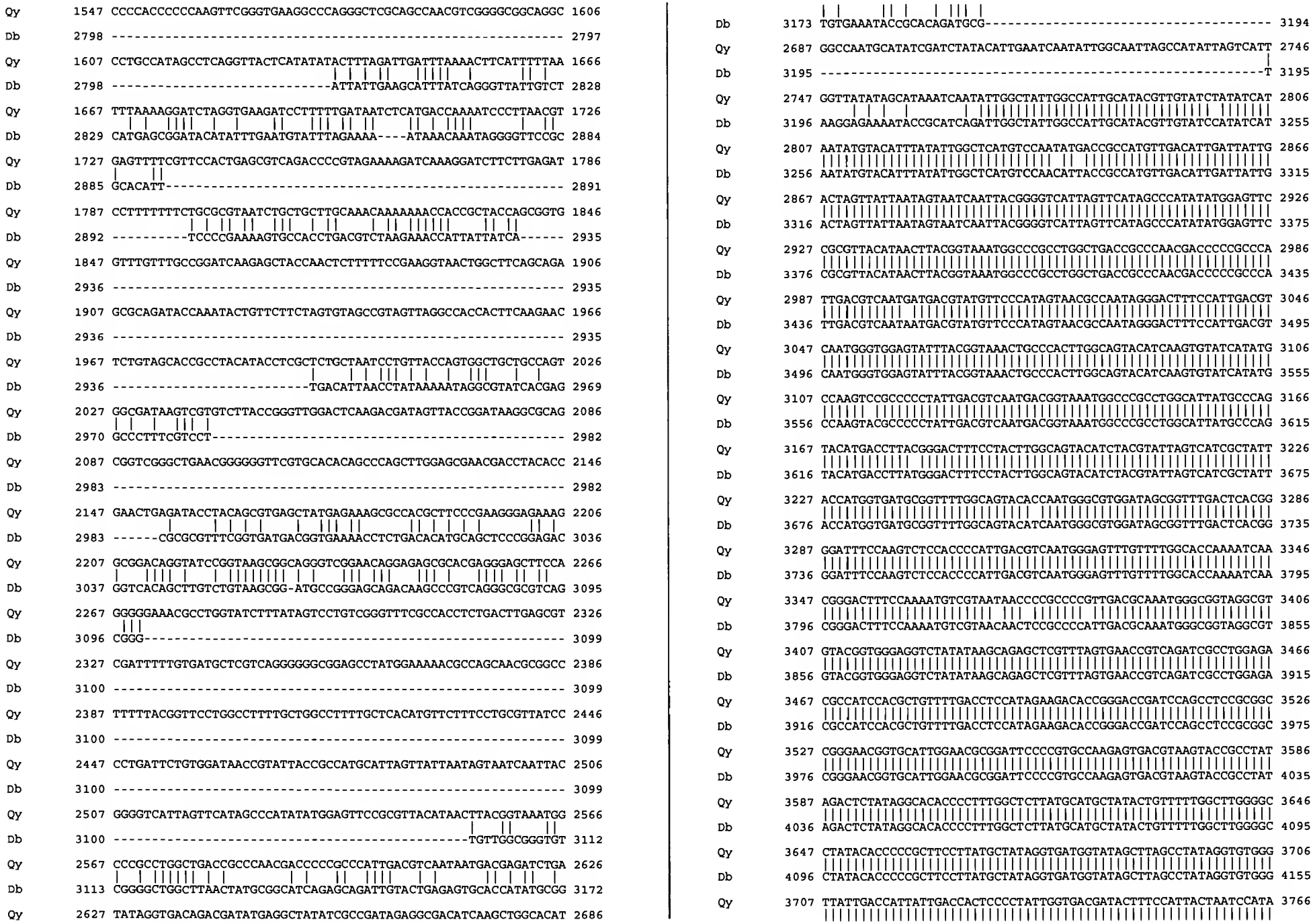

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ACCESSION   AX138936
VERSION     AX138936.1  GI:14274641
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Morsey,M.A. and Sheppard,M.G.
  TITLE     Growth hormone and growth hormone releasing hormone compositions
  JOURNAL   Patent: EP 1052286-A 55 15-NOV-2000;
            Pfizer Products Inc. (US)
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ORIGIN

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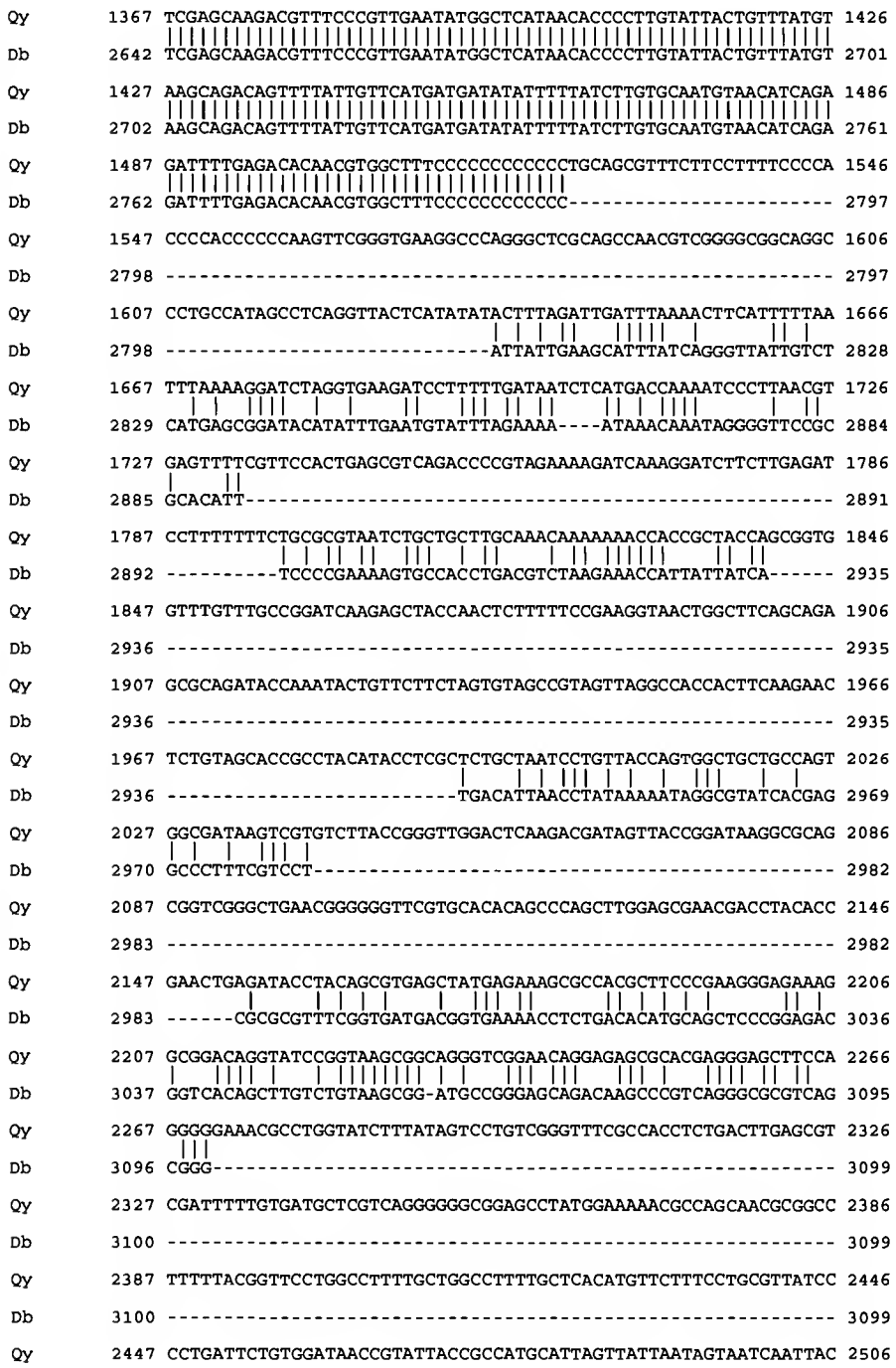

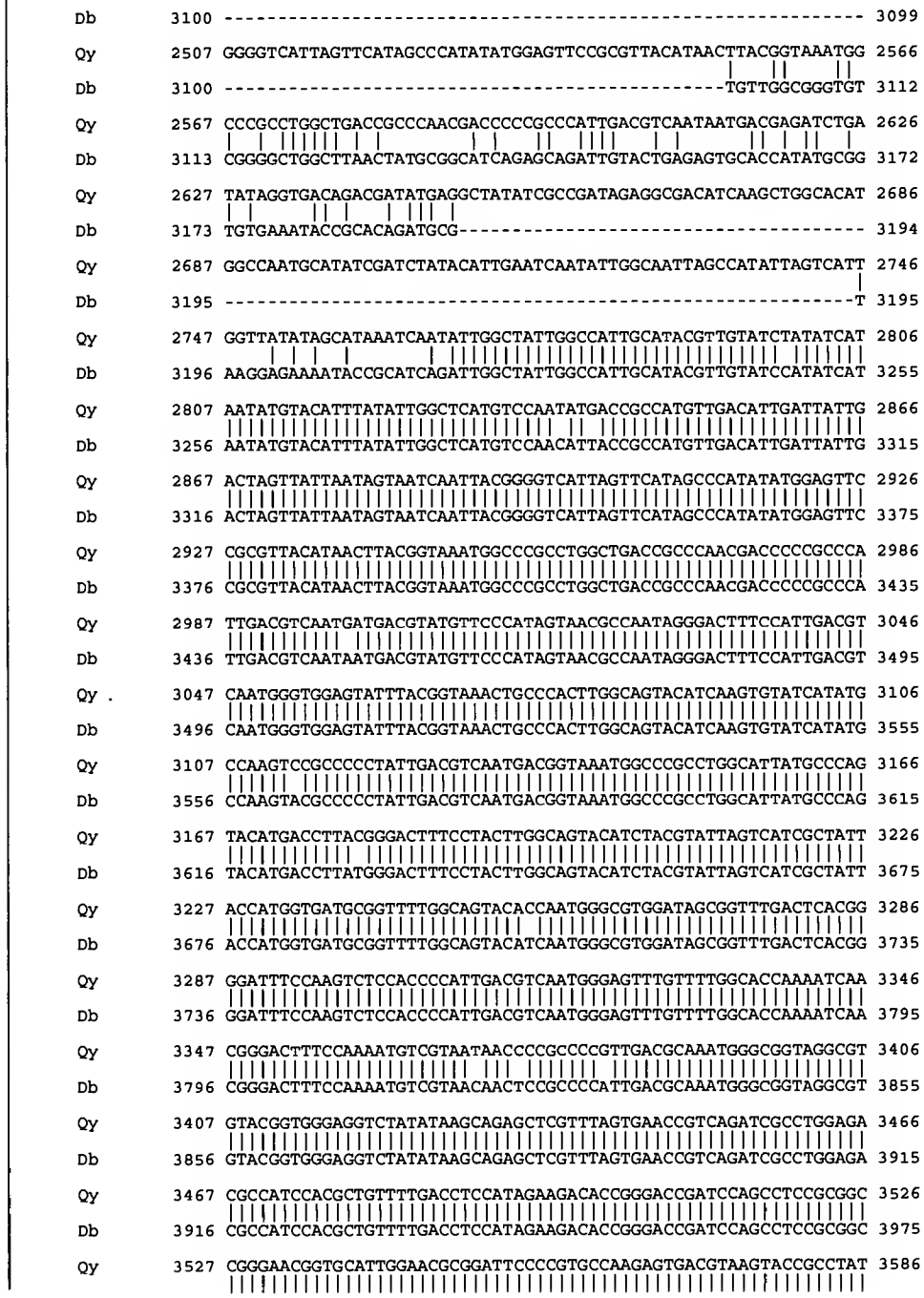

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Job time : 24056 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 12, 2004, 14:01:32 ; Search time 14701 Seconds
(without alignments)
13016.588 Million cell updates/sec

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Sequence: 1 attctgcagatatccagcac.....tcttattttaaaaaaccgga 6408

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	829.4	12.9	866	13	BQ682227	BQ682227 AGENCOURT
7	828.4	12.9	943	13	BQ677071	BQ677071 AGENCOURT
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14	772.2	12.1	939	13	BU179860	BU179860 AGENCOURT
15	762	11.9	940	13	BU191334	BU191334 AGENCOURT
16	760.2	11.9	766	12	BG765715	BG765715 602739734
c 17	758.6	11.8	1070	9	AJ281552	AJ281552 4A3A-P6F1
18	756	11.8	764	12	BI859609	BI859609 603388079
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c 36	687	10.7	1340	28	BZ572620	BZ572620 msh2_2721
c 37	685.6	10.7	896	28	BZ577395	BZ577395 msh2_5387
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c 39	682.4	10.6	733	28	BZ048997	BZ048997 jnr52g07.
c 40	682.2	10.6	860	28	BZ578295	BZ578295 msh2_5776
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c 43	677.4	10.6	1208	28	BZ577775	BZ577775 msh2_5567
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ALIGNMENTS

RESULT 1
AK014619
LOCUS AK014619 1932 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4633402C07 product:tyrosinase, full insert sequence.
ACCESSION AK014619
VERSION AK014619.1 GI:12852585
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1932)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES Location/Qualifiers

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/db_xref="MGI:1903271"
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/clone="4633402C07"
/tissue_type="skin"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"

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polyA_signal 1915. .1920
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polyA_site 1932
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ORIGIN

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Best Local Similarity 82.9%; Pred. No. 0;
Matches 1375; Conservative 0; Mismatches 271; Indels 12; Gaps 2;

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Qy       5409 GCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTCCCCTCTTCAGCTGATGT 5468

Db        995 ACGTAATCCTGGAAACCATGACAAAGCCAAAACCCCCAGGCTCCCATCTTCAGCAGATGT 1054

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Db       1055 GGAATTTTGTCTGAGTTTGACCCAGTATGAATCTGGATCAATGGATAGAACTGCCAATTT 1114

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Db       1115 CAGCTTTAGAAACACACTGGAAGGATTTGCCAGTCCACTCACAGGGATAGCAGATCCTTC 1174

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RESULT 2
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DEFINITION  AGENCOURT_6445513 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5539977
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ACCESSION   BM463960
VERSION     BM463960.1  GI:18513002
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1063)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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            Plate: LLAM12235  row: f  column: 10
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ORIGIN

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Db        993 GGGACCTTTACGGCGTATTC--TGGAAACATGACAATTCNGNA--CCCNAAGGTCCCCTC 1048

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RESULT 3
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DEFINITION  AGENCOURT_8076683 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089012
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ACCESSION   BU190117
VERSION     BU190117.1  GI:22704101
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
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                     NIH_MGC Library."
ORIGIN

  Query Match           13.6%;  Score 874.6;  DB 13;  Length 984;
  Best Local Similarity   96.6%;  Pred. No. 4.8e-240;
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Qy       4810 AACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGAGAGACGACTCTTG 4869
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Db        304 AACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGAGAGACGACTCTTG 363

Qy       4870 GTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATTTTTTGCCTACCTC 4929
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 GTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATTTTTTGCCTACCTC 423

Qy       4930 ACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGGGACCTATGGCCAA 4989
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 ACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGGGACCTATGGCCAA 483

Qy       4990 ATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGACCTCTTTGTCTGG 5049
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Db        484 ATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGACCTCTTTGTCTGG 543

Qy       5050 ATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATATGAAATCTGGAGAGACATT 5109
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Db        544 ATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATCTGAAATCTGGAGAGACATT 603

Qy       5110 GATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTTCTTGTTGCGGTGG 5169
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 GATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTTCTTGTTGCGGTGG 663

Qy       5170 GAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACTATTCCATATTGGGACTGG 5229
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Db        664 GAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACTATTCCATATTGGGACTGG 723

Qy       5230 CGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAGCACCCCACA 5289
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 CGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAGCACCCCCAC 783

Qy       5290 AATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCAGATTGTCTGTAGCCGA 5349
                |||||||||||||||| |||||||||||||||||||||||||||||| ||||||||||||
Db        784 AATCCTAACTTACTCACCCCAGCATCATTCTTCTCCTCTTGGCAGAATGTCTGTAGCCGA 843

Qy       5350 -TTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGG--AACGCCCGAGGGACCTTTA 5406
                 ||| |||||||||| ||||||||||||||||||||||   |    ||   ||||||||||
Db        844 TTTGAAGGAGTACACCAGCCATCAGTCTTTATGCAATGGGAACGCCCGAGGGGACCTTTA 903
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Qy       5407 CGGCG-TAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTCCCCTCTTCAGCTG 5464
              |||||  ||||||||||||||||||    ||||| ||| ||| | |  | || | ||  | |
Db        904 CGGCGTTAATCCTGGAAACCATGGACAATCCCGAAACCCCAAGGGCTCCCCCTCTTCAG 962


RESULT 4
BM557397
LOCUS       BM557397               1068 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6561703 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5547850
            5', mRNA sequence.
ACCESSION   BM557397
VERSION     BM557397.1  GI:18799358
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1068)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12255  row: n  column: 11
            High quality sequence stop: 643.
FEATURES             Location/Qualifiers
     source          1. .1068
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                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
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                     Technologies."
ORIGIN

  Query Match             13.3%;  Score 849.4;  DB 12;  Length 1068;
  Best Local Similarity   93.9%;  Pred. No. 9.6e-233;
  Matches  959;  Conservative    0;  Mismatches   53;  Indels    9;  Gaps    7;

Qy       4497 TGGTGGAATTCCGGGAAGAATGCTCCTGGCTGTTTTGTACTGCCTGCTGTGGAGTTTCCA 4556
              ||   | | |  ||||||||||||||||||||||||||||||||||||||||||||||||
Db         45 TGTGAGGACTAGAGGAAGAATGCTCCTGGCTGTTTTGTACTGCCTGCTGTGGAGTTTCCA 104

Qy       4557 GACCTCCGCTGGCCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAGAAGGA 4616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        105 GACCTCCGCTGGCCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAGAAGGA 164

Qy       4617 ATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGAGGTTC 4676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        165 ATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGAGGTTC 224

Qy       4677 CTGTCAGAATATCCTTCTGTCCAATGCACCACTTGGGCCTCAATTTCCCTTCACAGGGGT 4736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        225 CTGTCAGAATATCCTTCTGTCCAATGCACCACTTGGGCCTCAATTTCCCTTCACAGGGGT 284

Qy       4737 GGATGACCGGGAGTCGTGGCCTTCCGTCTTTTATAATAGGACCTGCCAGTGCTCTGGCAA 4796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        285 GGATGACCGGGAGTCGTGGCCTTCCGTCTTTTATAATAGGACCTGCCAGTGCTCTGGCAA 344

Qy       4797 CTTCATGGGATTCAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGA 4856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        345 CTTCATGGGATTCAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGA 404

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 GAGACGACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATT 464

Qy       4917 TTTTGCCTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGG 4976
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        465 TTTTGCCTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGG 524

Qy       4977 GACCTATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGA 5036
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Db        525 GACCTATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGA 584

Qy       5037 CCTCTTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATATGAAAT 5096
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Db        585 CCTCTTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGNGGGATCTGAAAT 644

Qy       5097 CTGGAGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTT 5156
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Db        645 CTGGAGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTT 704

Qy       5157 CTTGTTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACTATTCC 5216
              |||||||||||||||  | ||||||||||||||||||||||||||||||||||||||||||
Db        705 CTTGTTGCGGTGGGAAACAAGAATCCAGAAGCTGACAGGAGATGAAAACTTCACTATTCC 764

Qy       5217 ATATT-GGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACAT-GGGA 5274
              |||||  |||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        765 ATATTGGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGGA 824

Qy       5275 GGTCAGCACCCCA-CAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCA 5333
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Db        825 GGTCAGCACCCCACCAAATCTAAACTTACTCAGCCCAGCATCATTCTTCTTCTCTTGGCA 884

Qy       5334 GATTGTCTGTAGCCGA-TTGGAGGAGTACAACAGCCATCAGTC-TTTATGCAATGGAACG 5391
              ||||||||||| |||| |||||||||||||||| |||||||| |||||||||||||||||
Db        885 GATTGTCTGTAACCGATTTGGAGGAGTACAACAGGCATCAGTCTTTTATGCAATGGAACG 944

Qy       5392 CCCGAGGGACCTTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAA-CCCCAAGGCT 5450
              ||| ||||   |||   | |||||||||||||||||   ||| ||||| ||||||||||
Db        945 CCCAAGGGGATTTTTACGGGTAATCCTGGAAACCATGGACAATTCAGAACCCCCAAGGCT 1004

Qy       5451 CCCCTCTTCAGCTG---ATGTAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGTTC 5507
              ||||||  |   |||    |  |  |||  |   | || ||||||||||||   || | |
Db       1005 CCCCTCCTTCNCTGGATGTAAAATTTTTGCCTGAATTTGGACCCAATATGAAATCGGGTT 1064

Qy       5508 C 5508
              |
Db       1065 C 1065


RESULT 5
BU183039
LOCUS       BU183039               903 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_7932460 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6157206
            5', mRNA sequence.
ACCESSION   BU183039
VERSION     BU183039.1  GI:22697023
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
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           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLAM13502  row: l  column: 07
           High quality sequence stop: 683.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             13.1%;  Score 837;  DB 13;  Length 903;
  Best Local Similarity   97.6%;  Pred. No. 3.3e-229;
  Matches  880;  Conservative    0;  Mismatches   18;  Indels    4;  Gaps    3;

Qy       4552 TTCCAGACCTCCGCTGGCCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAG 4611
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TTCCAGACCTCCGCTGGCCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAG 60

Qy       4612 AAGGAATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGA 4671
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            61 AAGGAATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGA 120

Qy       4672 GGTTCCTGTCAGAATATCCTTCTGTCCAATGCACCACTTGGGCCTCAATTTCCCTTCACA 4731
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Db           121 GGTTCCTGTCAGAATATCCTTCTGTCCAATGCACCACTTGGGCCTCAATTTCCCTTCACA 180

Qy       4732 GGGGTGGATGACCGGGAGTCGTGGCCTTCCGTCTTTTATAATAGGACCTGCCAGTGCTCT 4791
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           181 GGGGTGGATGACCGGGAGTCGTGGCCTTCCGTCTTTTATAATAGGACCTGCCAGTGCTCT 240

Qy       4792 GGCAACTTCATGGGATTCAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGC 4851
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           241 GGCAACTTCATGGGATTCAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGC 300

Qy       4852 ACAGAGAGACGACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGAC 4911
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Db           301 ACAGAGAGACGACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGAC 360

Qy       4912 AAATTTTTTGCCTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCC 4971
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Db           361 AAATTTTTTGCCTACCTCACTTTAGCAAATCATACCATCAGCTCAGACTATGTCATCCCC 420

Qy       4972 ATAGGGACCTATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATT 5031
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Db           421 ATAGGGACCTATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATT 480

Qy       5032 TATGACCTCTTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATAT 5091
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Db           481 TATGACCTCTTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATCT 540

Qy       5092 GAAATCTGGAGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGA 5151
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Db           541 GAAATCTGGAGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGA 600

Qy       5152 CTCTTCTTGTTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACT 5211
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Db           601 CTCTTCTTGTTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACT 660

Qy       5212 ATTCCATATTGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATG 5271
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Db           661 ATTCCATATTGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATG 720

Qy       5272 G-GAGGTCAGCACCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTG 5330
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Db           721 GNGAGGTCAGCACCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTG 780

Qy       5331 GCAGATTGTCTGTAGCC-GATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGAA 5389
              |||||||||||||||| |||| |  |||||| ||||||||||||||||||||||||||||
Db           781 GCAGATTGTCTGTAGCCGGATTTGGAGAGTACCACAGCCATCAGTCTTTATGCAATGGAA 840

Qy       5390 CGCCCGAGGGA--CCTTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAG 5447
                |||| ||   | ||   |  ||||||||||||||||||||||||||||||||||| ||
Db           841 ACGCCGANGGNACCTTTACNGCGGTAATCCTGGAAACCATGACAAATCCAGAACCCCCAG 900

Qy       5448 GC 5449
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Db           901 GC 902


RESULT 6
BQ682227
LOCUS       BQ682227                866 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8208342 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6262799
            5', mRNA sequence.
ACCESSION   BQ682227
VERSION     BQ682227.1  GI:21794906
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 866)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2425  row: k  column: 24
            High quality sequence stop: 661.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             12.9%;  Score 829.4;  DB 13;  Length 866;
  Best Local Similarity   98.4%;  Pred. No. 5e-227;
  Matches  847;  Conservative    0;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       4509 GGGAAGAATGCTCCTGGCTGTTTTGTACTGCCTGCTGTGGAGTTTCCAGACCTCCGCTGG 4568
              | | |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db             2 GAGGAAGATGCTCCTGGCTGTTTTGTACTGCCTGCTGTGGAGTTTCCAGACCTCCGCTGG 61

Qy       4569 CCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAGAAGGAATGCTGTCCACC 4628
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            62 CCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAGAAGGAATGCTGTCCACC 121
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Qy       4629 GTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGAGGTTCCTGTCAGAATAT 4688
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Db        122 GTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGAGGTTCCTGTCAGAATAT 181

Qy       4689 CCTTCTGTCCAATGCACCACTTGGGCCTCAATTTCCCTTCACAGGGGTGGATGACCGGGA 4748
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Qy       4749 GTCGTGGCCTTCCGTCTTTTATAATAGGACCTGCCAGTGCTCTGGCAACTTCATGGGATT 4808
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Qy       4809 CAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGAGAGACGACTCTT 4868
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Db        302 CAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGAGAGACGACTCTT 361

Qy       4869 GGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATTTTTTGCCTACCT 4928
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Db        362 GGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATTTTTTGCCTACCT 421

Qy       4929 CACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGGGACCTATGGCCA 4988
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 CACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGGGACCTATGGCCA 481

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Qy       5049 GATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATATGAAATCTGGAGAGACAT 5108
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Qy       5109 TGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTTCTTGTTGCGGTG 5168
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Qy       5229 GCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAGCACCCCAC 5288
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Db        722 GCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAGCACCCCAC 781

Qy       5289 AAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCAGATTGTCTGTAG-CC 5347
             |||||||||||||||||||||||||||||||| |||||||||    |||||||||||| ||
Db        782 AAATCCTAACTTACTCAGCCCAGCATCATTCCTCTCCTCTTGNGCAATTGTCTGTAGCCC 841

Qy       5348 GATTGGAGGAGTACAACAGCC 5368
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Db        842 GATTGGAGGAGTACAACCGCC 862
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RESULT 7
BQ677071
LOCUS BQ677071 943 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8209637 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6272720 5', mRNA sequence.
ACCESSION BQ677071
VERSION BQ677071.1 GI:21789750
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 943)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2451 row: i column: 09
High quality sequence stop: 636.
FEATURES Location/Qualifiers
source 1. .943
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6272720"
/tissue_type="melanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_112"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 12.9%; Score 828.4; DB 13; Length 943;
Best Local Similarity 97.7%; Pred. No. 1e-226;
Matches 881; Conservative 0; Mismatches 15; Indels 6; Gaps 4;

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Qy       5089 TATGAAATCTGGAGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCAT 5148
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Db          1 TCTGAAATCTGGAGAGA-ATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCAT 59

Qy       5149 AGACTCTTCTTGTTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTC 5208
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 AGACTCTTCTTGTTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTC 119

Qy       5209 ACTATTCCATATTGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTAC 5268
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Db        120 ACTATTCCATATTGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTAC 179

Qy       5269 ATGGGAGGTCAGCACCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCT 5328
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 ATGGGAGGTCAGCACCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCT 239

Qy       5329 TGGCAGATTGTCTGTAGCCGATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGA 5388
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 TGGCAGATTGTCTGTAGCCGATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGA 299

Qy       5389 ACGCCCGAGGGACCTTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGG 5448
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 ACGCCCGAGGGACCTTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGG 359

Qy       5449 CTCCCCTCTTCAGCTGATGTAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGTTCC 5508
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CTCCCCTCTTCAGCTGATGTAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGTTCC 419

Qy       5509 ATGGATAAAGCTGCCAATTTCAGCTTTAGAAATACACTGGAAGGATTTGCTAGTCCACTT 5568
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Db        420 ATGGATAAAGCTGCCAATTTCAGCTTTAGAAATACACTGGAAGGATTTGCTAGTCCACTT 479

Qy       5569 ACTGGGATAGCGGATGCCTCTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAAT 5628
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 ACTGGGATAGCGGATGCCTCTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAAT 539

Qy       5629 GGAACAATGTCCCAGGTACAGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCATGCA 5688
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Db        540 GGAACAATGTCCCAGGTACAGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCATGCA 599

Qy       5689 TTTGTTGACAGTATTTTTGAGCAGTGGCTCCGAAGGCACCGTCCTCTTCAAGAAGTTTAT 5748
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Db        600 TTTGTTGACAGTATTTTTGAGCAGTGGCTCCAAAGGCACCGTCCTCTTCAAGAAGTTTAT 659

Qy       5749 CCAGAAGCCAATGCACCCATTGGACATAACCGGGAATCCTACATGGTTCCTTTTATACCA 5808
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Db        660 CCAGAAGCCAATGCACCCATTGGACATAACCGGGAATCCTACATGGTTCCTTTTATACCA 719

Qy       5809 CTGTACAGAAATGGTGATTTCTTTATTTCATCCAAAGATCTGGGCTATGACTATAGCTAT 5868
             ||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Db        720 CTGTACAGAAATGGTGATTTCTTTATTTCAT-CAAGGATCTGGGCTATGACTATAGCTAT 778

Qy       5869 CTACAAGATTCAGACCCAGACTCTTTTCAAGACTACATTAAGTCCTATTTGGAACAAG-C 5927
             |||  |||||||||||||||||||||| |||||||||||||||||||||||||||||| |
Db        779 CTANCAGATTCAGACCCAGACTCTTTTCNAGACTACATTAAGTCCTATTTGGAACAAGCC 838

Qy       5928 GAGTCGGATCTGGTCATGGCTCCTTGGGGCGGCGA---TGGTAGGGGCCGTCCTCACTGC 5984
             |||||||||||||||| |||||||||| || |    |   |||||| |||||||||
Db        839 GAGTCGGATCTGGTCATGCCTCCTTGGGGCCGCNAAATGGAANGGGGCCCTCCTCACTGG 898

Qy       5985 CC 5986
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Db        899 CC 900


RESULT 8
BQ424642
LOCUS       BQ424642                926 bp    mRNA    linear   EST 23-MAY-2002
DEFINITION  AGENCOURT_7926673 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6160409
            5', mRNA sequence.
ACCESSION   BQ424642
VERSION     BQ424642.1  GI:21119957
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 926)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13511  row: a  column: 18
            High quality sequence stop: 628.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6160409"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             12.8%;  Score 817.4;  DB 13;  Length 926;
  Best Local Similarity   96.5%;  Pred. No. 1.5e-223;
  Matches  888;  Conservative    0;  Mismatches   24;  Indels    8;  Gaps    5;

Qy       4863 ACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATTTTTTGC 4922
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db          9 ACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGA-AAATTTTTTGC 67

Qy       4923 CTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGGGACCTA 4982
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         68 CTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGGGACCTA 127

Qy       4983 TGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGACCTCTT 5042
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 TGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGACCTCTT 187

Qy       5043 TGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATATGAAATCTGGAG 5102
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        188 TGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATCTGAAATCTGGAG 247

Qy       5103 AGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTTCTTGTT 5162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        248 AGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTTCTTGTT 307

Qy       5163 GCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACTATTCCATATTG 5222
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACTATTCCATATTG 367

Qy       5223 GGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAGCA 5282
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAGCA 427

Qy       5283 CCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCAGATTGTCTG 5342
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        428 CCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCAGATTGTCTG 487

Qy       5343 TAGCCGATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGAACGCCCGAGGGACC 5402
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        488 TAGCCGATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGAACGCCCGAGGGACC 547

Qy       5403 TTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTCCCCTCTTCAGC 5462
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 TTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTCCCCTCTTCAGC 607

Qy       5463 TGATGTAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGTTCCATGGATAAAGCTGC 5522
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        608 TGATGTAGAATTTTGCCTGAG-TTGACCCAATATGAATCTGGTTCCATGGATAAAGCTGC 666

Qy       5523 CAATTTCAGCTTTAGAAATACACTGGAAGGATTTGCTAGTCCACTTACTGGGATAGCGGA 5582
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db        667 CAATTTCAGCTTTAGAAATACACTGGGAGGATTTGCTAGTCCACTTACTGGGATAGCGGA 726

Qy       5583 TGCCTCTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAATGGAACAATGT-CCC 5641
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Db        727 TGCCTCTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAATGGGACNATGTCCCC 786

Qy       5642 AGGTACAGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCATGCATTTGTTG---ACA 5698
             |||||||||||||||||||||||||||||||||||||||||||||||||||||    |
Db        787 AGGTACAGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCATGCATTTGTTGGACAGT 846

Qy       5699 GTATTTTTGAGCAGTGGCTCCGAAGGCACCGTCC--TCTTCAAGAAGTTTATCCAGAAGC 5756
                 |||||||||||||||||| || |   ||| |    ||  |||  ||||||||||
Db        847 AATTTTTTGAGCAGTGGCTCCAAAAGGCACGTNCCTCTTTTCAGAGTTTTATCCAGAAAG 906

Qy       5757 CAATGCACCCATTGGACATA 5776
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Db        907 CANTGCACCCATTGGACATA 926


RESULT 9
BQ424713
LOCUS       BQ424713                908 bp    mRNA    linear   EST 23-MAY-2002
DEFINITION  AGENCOURT_7926435 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6160418
            5', mRNA sequence.
ACCESSION   BQ424713
VERSION     BQ424713.1  GI:21120028
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1  (bases 1 to 908)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13511  row: b  column: 03
            High quality sequence stop: 628.
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                     /clone="IMAGE:6160418"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_72"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             12.4%;  Score 793.4;  DB 13;  Length 908;
  Best Local Similarity   96.9%;  Pred. No. 1.3e-216;
  Matches  863;  Conservative    0;  Mismatches   21;  Indels    7;  Gaps    5;

Qy       4852 ACAGAGAGACGACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGAC 4911
             |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 ACAGAGAGACGACTCTTGGTGAGAAG-AACATCTTCGATTTGAGTGCCCCAGAGAAGGAC 59

Qy       4912 AAATTTTTTGCCTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCC 4971
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 AAATTTTTTGCCTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCC 119

Qy       4972 ATAGGGACCTATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATT 5031
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 ATAGGGACCTATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATT 179

Qy       5032 TATGACCTCTTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATAT 5091
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Db        180 TATGACCTCTTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATCT 239

Qy       5092 GAAATCTGGAGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGA 5151
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Db        240 GAAATCTGGAGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGA 299

Qy       5152 CTCTTCTTGTTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACT 5211
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 CTCTTCTTGTTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTCACT 359

Qy       5212 ATTCCATATTGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATG 5271
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Db        360 ATTCCATATTGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATG 419

Qy       5272 GGAGGTCAGCACCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGG 5331
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Db        420 GGAGGTCAGCACCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGG 479

Qy       5332 CAGATTGTCTGTAGCCGATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGAACG 5391
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Db        480 CAGATTGTCTGTAGCCGATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGAACG 539

Qy       5392 CCCGAGGGACCTTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTC 5451
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Db        540 CCCGAGGGACCTTTACGGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTC 599

Qy       5452 CCCTCTTCAGCTGATGTAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGTTCCATG 5511
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Db        600 CCCTCTTCAGCTGATGTAGAATTTTGCCTGAG-TTGACCCAATATGAATCTGGTTCCATG 658

Qy       5512 GATAAAGCTGCCAATTTCAGCTTTAGAAATACACT-GGAAGGATTTGCTAGTCCACTTAC 5570
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Qy       5571 T-GGGATAGCGGATGCCTCTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAATG 5629
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Db        719 TGGGGATAGCGGATGCCTCTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAATG 778

Qy       5630 GAACAATGTCCCAGGTACAGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCATGCAT 5689
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Db        779 GAACAATGTCCCAGGTACAGGGATCTGCCAACGATCCTATCTTCCCTTCTCACCATGCAT 838

Qy       5690 TTGTTG---ACAGTATTTTTGAGCAGTGGCTCCGAAGGCACCGTCCTCTTC 5737
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Db        839 TTGGTGGACAGGATTTTTTTGAGCAGTGGGCTCCAAAGGGACCGTCCCTTC 889


RESULT 10
BG575202
LOCUS       BG575202                902 bp    mRNA    linear   EST 10-APR-2001
DEFINITION  602597740F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4706552 5',
            mRNA sequence.
ACCESSION   BG575202
VERSION     BG575202.1  GI:13582855
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 902)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10574  row: p  column: 09
            High quality sequence stop: 869.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_87"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             12.4%;  Score 791.8;  DB 12;  Length 902;
  Best Local Similarity   96.1%;  Pred. No. 3.7e-216;
  Matches  833;  Conservative    0;  Mismatches   32;  Indels    2;  Gaps    2;

Qy       4497 TGGTGGAATTCCGGGAAGAATGCTCCTGGCTGTTTTGTACTGCCTGCTGTGGAGTTTCCA 4556
             ||   | | |  ||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 TGTGAGGACTAGAGGAAGAATGCTCCTGGCTGTTTTGTACTGCCTGCTGTGGAGTTTCCA 95
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Qy       4557 GACCTCCGCTGGCCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAGAAGGA 4616
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 GACCTCCGCTGGCCATTTCCCTAGAGCCTGTGTCTCCTCTAAGAACCTGATGGAGAAGGA 155

Qy       4617 ATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGAGGTTC 4676
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Db        156 ATGCTGTCCACCGTGGAGCGGGGACAGGAGTCCCTGTGGCCAGCTTTCAGGCAGAGGTTC 215

Qy       4677 CTGTCAGAATATCCTTCTGTCCAATGCACCACTTGGGCCTCAATTTCCCTTCACAGGGGT 4736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CTGTCAGAATATCCTTCTGTCCAATGCACCACTTGGGCCTCAATTTCCCTTCACAGGGGT 275

Qy       4737 GGATGACCGGGAGTCGTGGCCTTCCGTCTTTTATAATAGGACCTGCCAGTGCTCTGGCAA 4796
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Db        276 GGATGACCGGGAGTCGTGGCCTTCCGTCTTTTATAATAGGACCTGCCAGTGCTCTGGCAA 335

Qy       4797 CTTCATGGGATTCAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGA 4856
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Db        336 CTTCATGGGATTCAACTGTGGAAACTGCAAGTTTGGCTTTTGGGGACCAAACTGCACAGA 395

Qy       4857 GAGACGACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATT 4916
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Db        396 GAGACGACTCTTGGTGAGAAGAAACATCTTCGATTTGAGTGCCCCAGAGAAGGACAAATT 455

Qy       4917 TTTTGCCTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGG 4976
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Db        456 TTTTGCCTACCTCACTTTAGCAAAGCATACCATCAGCTCAGACTATGTCATCCCCATAGG 515

Qy       4977 GACCTATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGA 5036
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Db        516 GACCTATGGCCAAATGAAAAATGGATCAACACCCATGTTTAACGACATCAATATTTATGA 575

Qy       5037 CCTCTTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATATGAAAT 5096
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 CCTCTTTGTCTGGATGCATTATTATGTGTCAATGGATGCACTGCTTGGGGGATCTGAAAT 635

Qy       5097 CTGGAGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTT 5156
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Db        636 CTGGAGAGACATTGATTTTGCCCATGAAGCACCAGCTTTTCTGCCTTGGCATAGACTCTT 695

Qy       5157 CTTGTTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAAC-TTCACTATTC 5215
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Db        696 CTTGTTGCGGTGGGAACAAGAAATCCAGAAGCTGACAGGAGATGAAAACTTTCACTATTC 755

Qy       5216 CATATTGGGACTGGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACAT-GGGA 5274
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Db        756 CATATTGGGACTGGCGGGATGCAGAACAGTGTGACATTTGCACAGATGAGTACATGGGGA 815

Qy       5275 GGTCAGCACCCCACAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCAG 5334
             ||||||  ||| | || ||  |  | |||||||||||||||||||||||||||| |||||
Db        816 GGTCAGACCCCAAAAATTCTAAGTTAACTCAGCCCAGCATCATTCTTCTCCTCTGGGCAG 875

Qy       5335 ATTGTCTGTAGCCGATTGGAGGAGTAC 5361
             | |         |||| ||||||||||
Db        876 AATTGTCTGTAGCGATGGGAGGAGTAC 902


RESULT 11
BG576440
LOCUS       BG576440                965 bp    mRNA    linear   EST 10-APR-2001
DEFINITION  602595683F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4708629 5',
            mRNA sequence.
ACCESSION   BG576440
VERSION     BG576440.1  GI:13584093
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 965)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10580  row: f  column: 22
            High quality sequence stop: 737.
FEATURES             Location/Qualifiers
     source          1. .965
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4708629"
                     /tissue_type="mammary adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_87"
                     /note="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             12.3%;  Score 787.6;  DB 12;  Length 965;
  Best Local Similarity   94.1%;  Pred. No. 6.3e-215;
  Matches  886;  Conservative    0;  Mismatches   44;  Indels   12;  Gaps    6;

Qy       5228 GGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAGCACCCCA 5287
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Db         23 GGCGGGATGCAGAAAAGTGTGACATTTGCACAGATGAGTACATGGGAGGTCAGCACCCCA 82

Qy       5288 CAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCAGATTGTCTGTAGCC 5347
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 CAAATCCTAACTTACTCAGCCCAGCATCATTCTTCTCCTCTTGGCAGATTGTCTGTAGCC 142

Qy       5348 GATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGAACGCCCGAGGGACCTTTAC 5407
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 GATTGGAGGAGTACAACAGCCATCAGTCTTTATGCAATGGAACGCCCGAGGGACCTTTAC 202

Qy       5408 GGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTCCCCTCTTCAGCTGATG 5467
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Db        203 GGCGTAATCCTGGAAACCATGACAAATCCAGAACCCCAAGGCTCCCCTCTTCAGCTGATG 262

Qy       5468 TAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGTTCCATGGATAAAGCTGCCAATT 5527
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Db        263 TAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGTTCCATGGATAAAGCTGCCAATT 322

Qy       5528 TCAGCTTTAGAAATACACTGGAAGGATTTGCTAGTCCACTTACTGGGATAGCGGATGCCT 5587
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Db        323 TCAGCTTTAGAAATACACTGGAAGGATTTGCTAGTCCACTTACTGGGATAGCGGATGCCT 382

Qy       5588 CTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAATGGAACAATGTCCCAGGTAC 5647
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Db        383 CTCAAAGCAGCATGCACAATGCCTTGCACATCTATATGAATGGAACAATGTCCCAGGTAC 442

Qy       5648 AGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCATGCATTTGTTGACAGTATTTTTG 5707
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Db        443 AGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCATGCATTTGTTGACAGTATTTTTG 502

Qy       5708 AGCAGTGGCTCCGAAGGCACCGTCCTCTTCAAGAAGTTTATCCAGAAGCCAATGCACCCA 5767
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        503 AGCAGTGGCTCCAAAGGCACCGTCCTCTTCAAGAAGTTTATCCAGAAGCCAATGCACCCA 562

Qy       5768 TTGGACATAACCGGGAATCCTACATGGTTCCTTTTATACCACTGTACAGAAATGGTGA-T 5826
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Db        563 TTGGACATAACCGGGAATCCTACATGGTTCCTTTTATACCACTGTACAGAAATGGTGACT 622

Qy       5827 TTCTTTATTTCATCCAAAGATCTGGGCTATGACTATAGCTATCTACAAGATTCAGACCCA 5886
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Db        623 TTCTTTATTTCATCCAAAGATCTGGGCTATGACTATAGCTATCTACAAGATTCAGACCCA 682

Qy       5887 GACTCTTTTCAAGACTACATTAAGTCCTATTTGGAACAAGCGAGTCGGATCTGGTCATGG 5946
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 GACTCTTTTCAAGACTACATTAAGTCCTATTTGGAACAAGCGAGTCGGATCTGGTCATGG 742

Qy       5947 CTCCTTGGGGCGGCG-ATGGTAGGGGCCGTCCTCACTGCCCTGCTGGCAGGGCTTGTGAG 6005
             |||||||| |||||| | ||||||||||||||||||||||||||||||||||| |||||
Db        743 CTCCTTGGAGCGGCGCAAGGTAGGGGCCGTCCTCACTGCCCTGCTGGCAGGGCTGGTGAG 802

Qy       6006 CTTGCTGTGTCGTCACAAGAGAA----AGCAGCTTCCTGAAGAAAAGCAGCCACTC---C 6058
             |||||||||||||||||||||||    ||| |      | ||||||||||||||   |
Db        803 CTTGCTGTGTCGTCACAAGAGAAAAACAGCCCCCCTTGAAGAAAAAGCAGCCACTCCCTC 862

Qy       6059 TCATGGAGAAAGAGGATTACCACAGCTTGTATC-AGAGCCATTTATAAAAGGCTTA--GG 6115
                |  ||  |||||  |||||||||||||| |||||||| ||||| | |  ||  |
Db        863 ATGGCGCAAAGAAGGATACCCACAGCTTGTATCAAGAGCCATATATAACACGGCTAAGGC 922

Qy       6116 CAATAGAGTAGGGCCAAAAAGCCTGACCTCACTCTAACTCAA 6157
                | | |||   |||||||||  |    || ||||||||||||
Db        923 AATTCGAGGTAGGCCAAAAAAGCGTGACTAACTCTAACTCAA 964
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RESULT 12
AJ281480/c

LOCUS	AJ281480 1004 bp mRNA linear EST 30-JUN-2000
DEFINITION	4A3A-P4G8-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P4G8, mRNA sequence.
ACCESSION	AJ281480
VERSION	AJ281480.1 GI:6929360
KEYWORDS	EST.
SOURCE	Anopheles gambiae (African malaria mosquito)
ORGANISM	Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE	1 (bases 1 to 1004)
AUTHORS	Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C., Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B. and Kafatos,F.C.
TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
MEDLINE	20300950
PUBMED	10841561
COMMENT	Contact: Dimopoulos G Fotis C. Kafatos laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany.

FEATURES Location/Qualifiers

source 1. .1004
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4a r/r"
/db_xref="taxon:7165"
/clone="4A3A-P4G8"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH10B"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN

Query Match 12.3%; Score 786.6; DB 9; Length 1004;
Best Local Similarity 99.4%; Pred. No. 1.3e-214;
Matches 789; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy       1615 AGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 1674
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Db        794 AGACCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAG 735

Qy       1675 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 1734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 GATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTC 675

Qy       1735 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 1794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        674 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT 615

Qy       1795 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 1854
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Db        614 TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTT 555

Qy       1855 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 1914
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Db        554 GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGAT 495

Qy       1915 ACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 1974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        494 ACCAAATACTGTTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGC 435

Qy       1975 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 2034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        434 ACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA 375

Qy       2035 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 2094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        374 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGG 315

Qy       2095 CTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 2154
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        314 CTGAACGGGGGGTTCGTGCANACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 255

Qy       2155 ATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 2214
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Db        254 ATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAG 195

Qy       2215 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 2274
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Db        194 GTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAA 135

Qy       2275 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 2334
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Db        134 CGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTT 75

Qy       2335 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 2394
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Db          74 GTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACG 15

Qy       2395 GTTCCTGGCCTTTT 2408
              ||||||||||||||
Db          14 GTTCCTGGCCTTTT 1
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RESULT 13
AJ281449/c

LOCUS	AJ281449 800 bp mRNA linear EST 30-JUN-2000
DEFINITION	4A3A-P4D5-F Anopheles gambiae immune competent 4A3A Anopheles gambiae cDNA clone 4A3A-P4D5, mRNA sequence.
ACCESSION	AJ281449
VERSION	AJ281449.1 GI:6929329
KEYWORDS	EST.
SOURCE	Anopheles gambiae (African malaria mosquito)
ORGANISM	Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
REFERENCE	1 (bases 1 to 800)
AUTHORS	Dimopoulos,G., Casavant,T.L., Chang,S., Scheetz,T., Roberts,C.,

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            Donohue,M., Schultz,J., Benes,V., Bork,P., Ansorge,W., Soares,M.B.
            and Kafatos,F.C.
  TITLE     Anopheles gambiae pilot gene discovery project: identification of
            mosquito innate immunity genes from expressed sequence tags
            generated from immune-competent cell lines
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
  MEDLINE   20300950
   PUBMED   10841561
COMMENT     Contact: Dimopoulos G
            Fotis C. Kafatos laboratory
            European Molecular Biology Laboratory
            Meyerhofstrasse 1, 69117 Heidelberg, Germany.
FEATURES             Location/Qualifiers
     source          1. .800
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                     /mol_type="mRNA"
                     /strain="4a r/r"
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                     /clone="4A3A-P4D5"
                     /cell_line="immune competent 4A3A"
                     /lab_host="E. coli DH10B"
                     /clone_lib="Anopheles gambiae immune competent 4A3A"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from
                     forward priming site which reads from the 3' end of the
                     cDNA. The 4A3A is a directionally cloned and normalized
                     cDNA library that was constructed from the 4A3A cell line
                     oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
                     (1996) : Normalization and Subtraction: Two approaches To
                     Facilitate Gene Discovery, Genome Research 6, 791-806."
ORIGIN

  Query Match             12.2%;  Score 779.4;  DB 9;  Length 800;
  Best Local Similarity   99.2%;  Pred. No. 1.3e-212;
  Matches  783;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1636 ACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTT 1695
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Db        800 ACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTT 741

Qy       1696 TGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCC 1755
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Db        740 TGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCC 681

Qy       1756 CGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTT 1815
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        680 CGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTT 621

Qy       1816 GCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAAC 1875
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Db        620 GCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAAC 561

Qy       1876 TCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGT 1935
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Db        560 TCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGT 501

Qy       1936 GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCT 1995
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 GTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCT 441

Qy       1996 GCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGA 2055
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Db        440 GCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGA 381

Qy       2056 CTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCAC 2115
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Db        380 CTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCAC 321

Qy       2116 ACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATG 2175
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Db        320 ACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATG 261

Qy       2176 AGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGT 2235
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Db        260 AGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGT 201

Qy       2236 CGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCC 2295
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Db        200 CGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCC 141

Qy       2296 TGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCG 2355
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Db        140 TGTCGGGTTTCGCCACCTCTGACTTGAGCGTCTATTTTTGTGATGCTCGTCAGGGGGGCG 81

Qy       2356 GAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCC 2415
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Db          80 GAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCC 21

Qy       2416 TTTTGCTCA 2424
                 ||| |
Db          20 GCAAGCTTA 12


RESULT 14
BU179860
LOCUS       BU179860                939 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_8110331 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6266889
            5', mRNA sequence.
ACCESSION   BU179860
VERSION     BU179860.1  GI:22693844
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2436  row: f  column: 10
            High quality sequence stop: 606.
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                     /clone_lib="NIH_MGC_112"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             12.1%;  Score 772.2;  DB 13;  Length 939;
  Best Local Similarity   93.0%;  Pred. No. 1.7e-210;
  Matches  863;  Conservative    0;  Mismatches   56;  Indels    9;  Gaps    5;

Qy       5446 AGGCTCCCCTCTTCAGCTGATGTAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGT 5505
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Db          1 AGGCTCCCCTCTTCAGCTGATGTAGAATTTTGCCTGAGTTTGACCCAATATGAATCTGGT 60
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Qy       5506 TCCATGGATAAAGCTGCCAATTTCAGCTTTAGAAATACACTGGAAGGATTTGCTAGTCCA 5565
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Db        181 AATGGAACAATGTCCCAGGTACAGGGATCTGCCAACGATCCTATCTTCCTTCTTCACCAT 240

Qy       5686 GCATTTGTTGACAGTATTTTTGAGCAGTGGCTCCGAAGGCACCGTCCTCTTCAAGAAGTT 5745
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Db        241 GCATTTGTTGACAGTATTTTTGAGCAGTGGCTCCAAAGGCACCGTCCTCTTCAAGAAGTT 300

Qy       5746 TATCCAGAAGCCAATGCACCCATTGGACATAACCGGGAATCCTACATGGTTCCTTTTATA 5805
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Db        421 TATCTACAAGATTCAGACCCAGACTCTTTTCAAGACTACATTAAGTCCTATTTGGAACAA 480

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Db        481 GCGAGTCGGATCTGGTCATGGCTCCTTGGGGCGGCGATGGTAGGGGCCGTCCTCACTGCC 540

Qy       5986 CTGCTGGCAGGGCTTGTGAGCTTGCTGTGTCGTCACAAGAGAAAGCAGCTTCCTGAAGAA 6045
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Db        541 CTGCTGGCAGGGCTTGTGAGCTTGCTGTGTCGTCACAAGAGAAAGCAGCTTCCTGAAGAA 600

Qy       6046 AAGCAGCCACTCCTCATGGAGAAAGAGGATTACCACAGCTTGTATCAGAGCCATTTATAA 6105
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Db        601 AAGCAGCCACTCCTCATGGAGAAAGAGGATTACCACAGCTTGTATCAGAGCCATTTATAA 660

Qy       6106 AAGGCTTAGGCAATAGAGTAGGGCCAAAAAGCCTGACCTCACTCTAACTCAAAGTAATGT 6165
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Qy       6166 CCAGGTTCCC---AGAGAATATCTGCTGGTATTTTTCTGTAAAGACCATTT---GCAAAA 6219
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Db        721 CCAGGTTTCCCAGAGAATATCTNGCTGGTATTTTTTCTGTNAAGACCATTTTGCAAAAAT 780

Qy       6220 TTGTAACCTAATACAAAGTGTAG-CCTTCTTCCAACTCAGGTAGAACACA-CCTGTCTTT 6277
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Qy       6337 AAGGATGCTATTTGGTAATGAGGAACTG 6364
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Db        901 AGGAAAGGGATGCCTAATTGGGGAAATG 928


RESULT 15
BU191334
LOCUS       BU191334                940 bp    mRNA    linear   EST 04-SEP-2002
DEFINITION  AGENCOURT_8106643 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6253948
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ACCESSION   BU191334
VERSION     BU191334.1  GI:22705318
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 940)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2402  row: k  column: 05
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                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             11.9%;  Score 762;  DB 13;  Length 940;
  Best Local Similarity   98.4%;  Pred. No. 1.5e-207;
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